

FIGURE 1

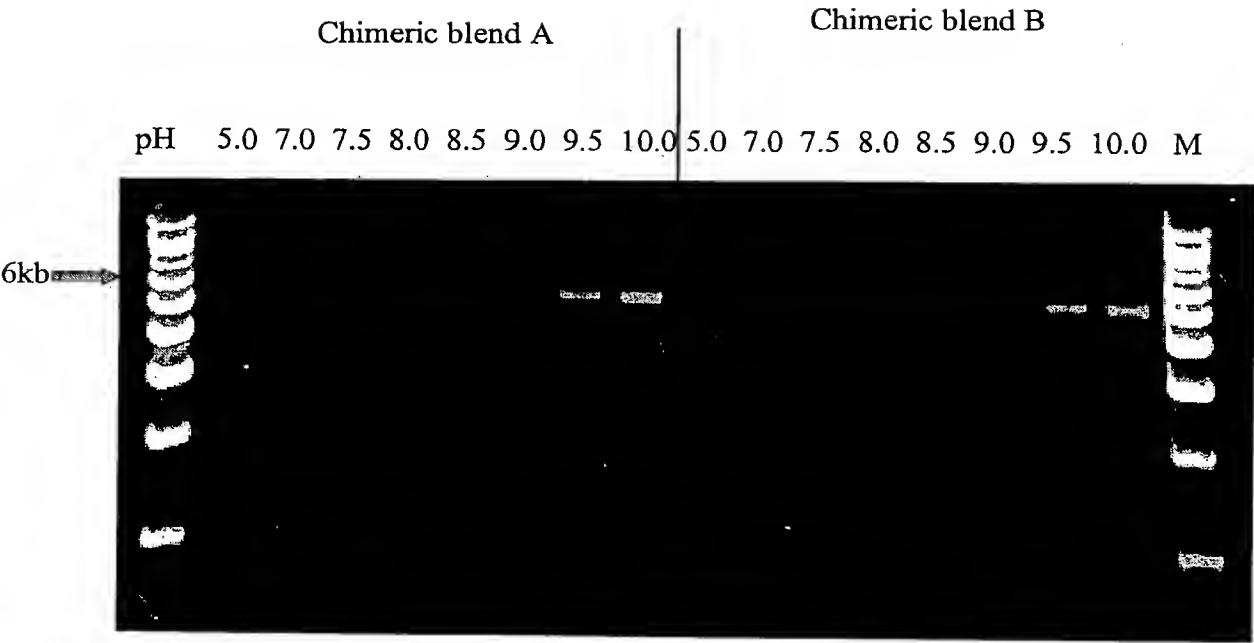


FIGURE 2

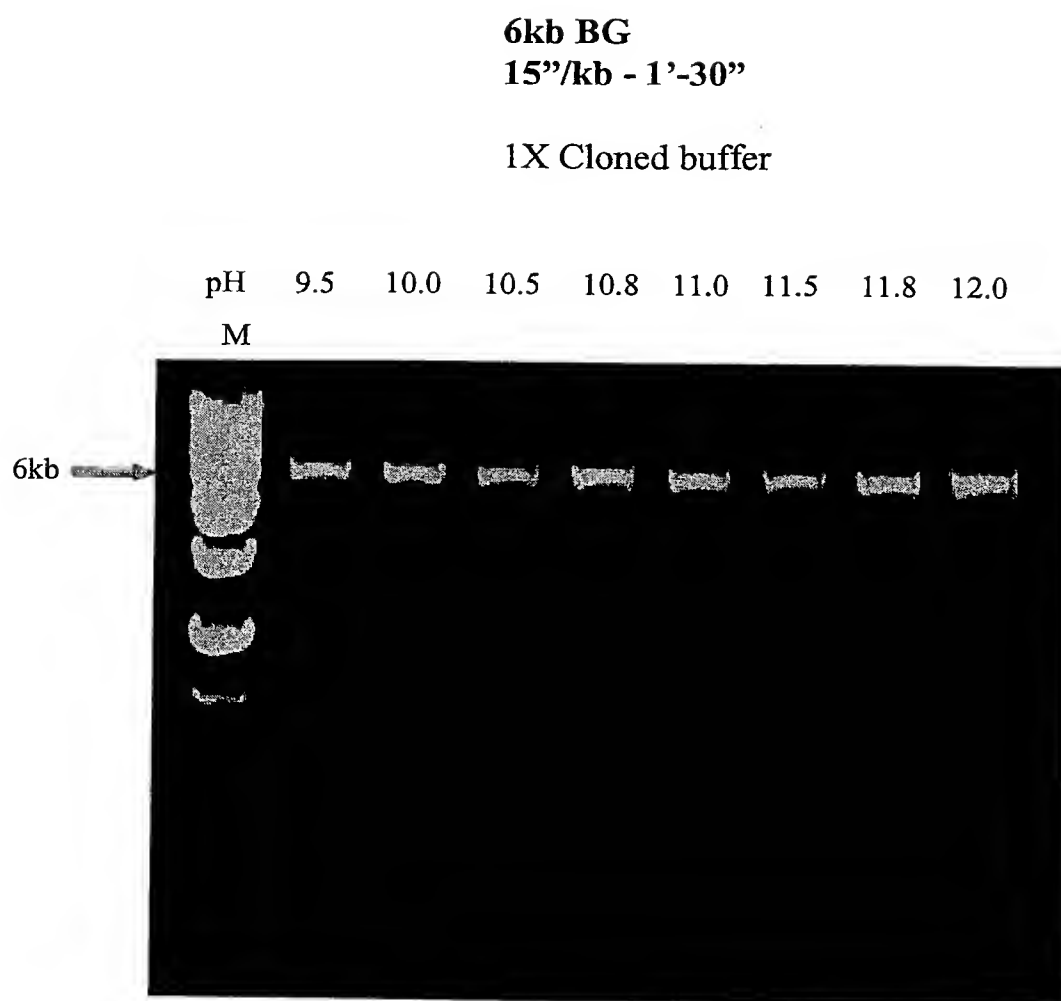


FIGURE 3

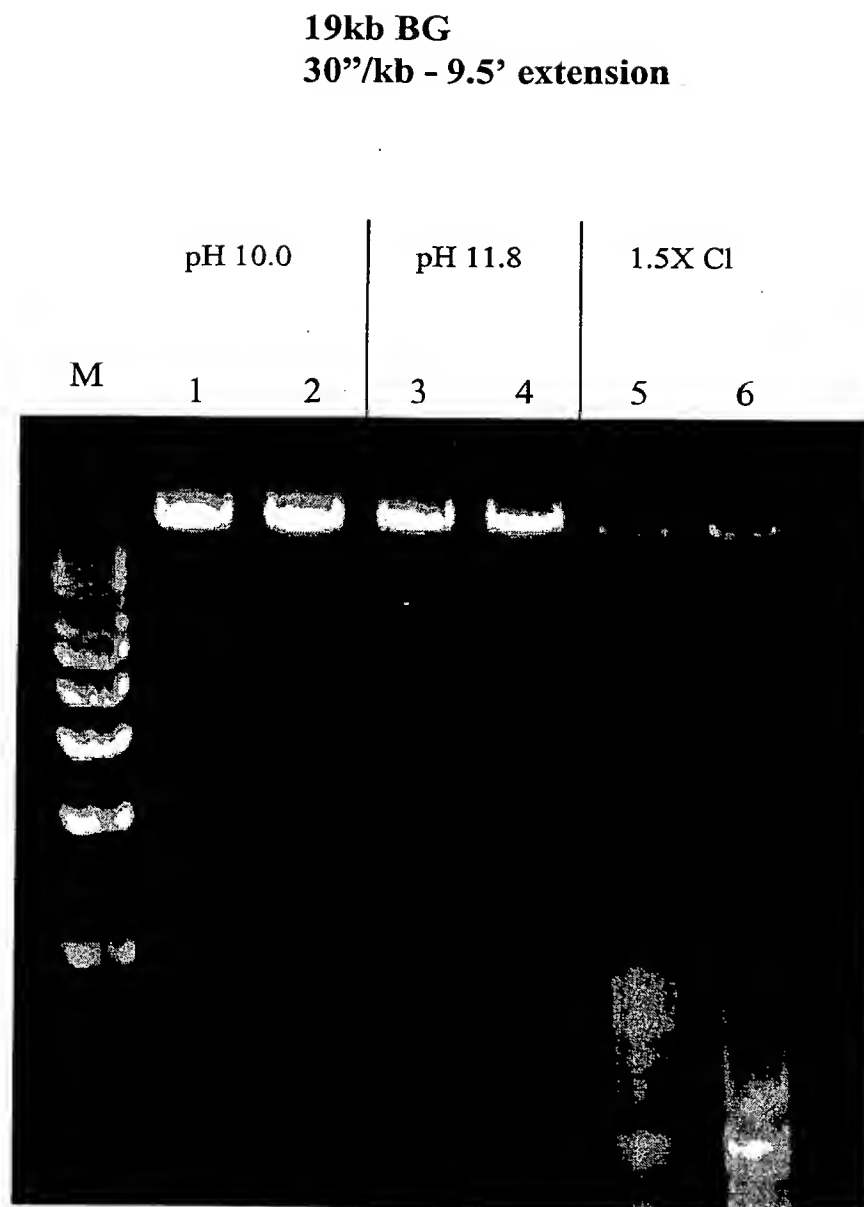


FIGURE 4

19kb BG
30''/kb - 9.5' extension

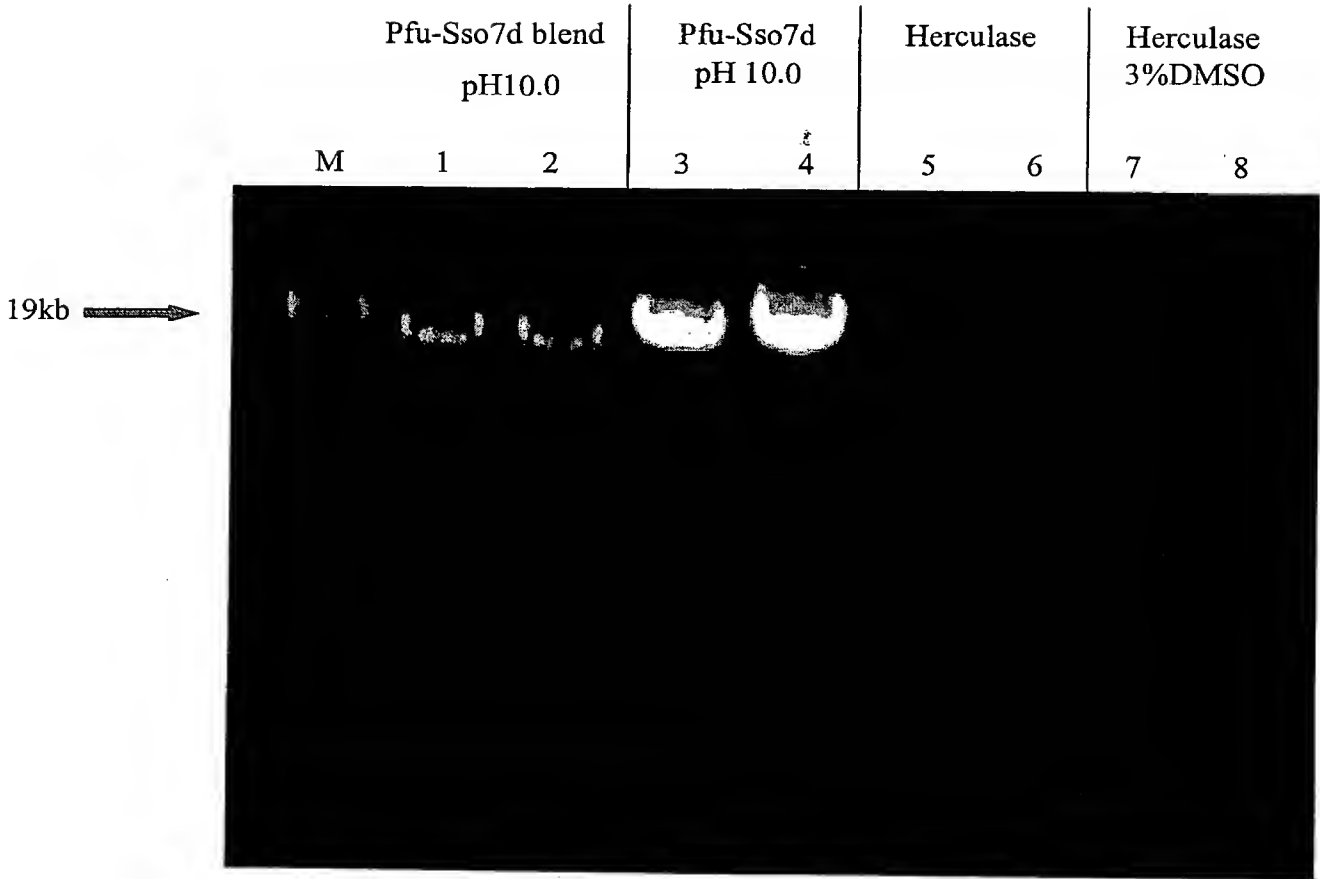


FIGURE 5

19kb BG
30"/kb - 9.5' extension

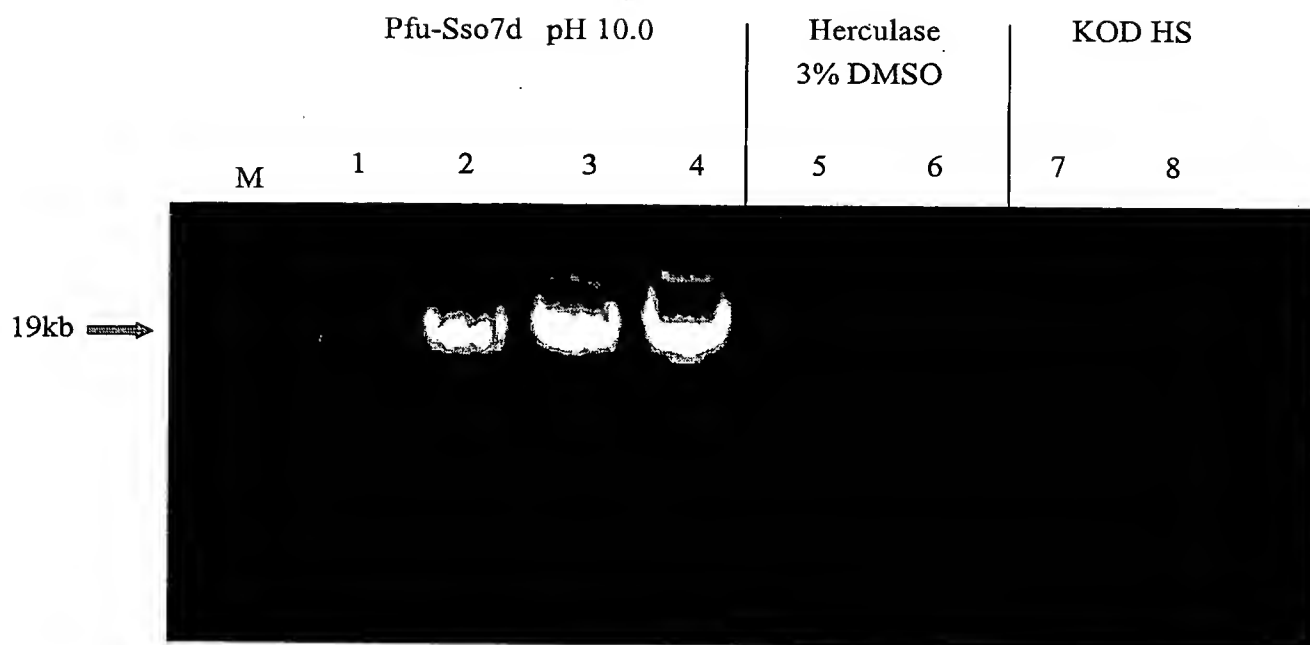


FIGURE 6

900bp H α AT
1''/kb - 1'' extension

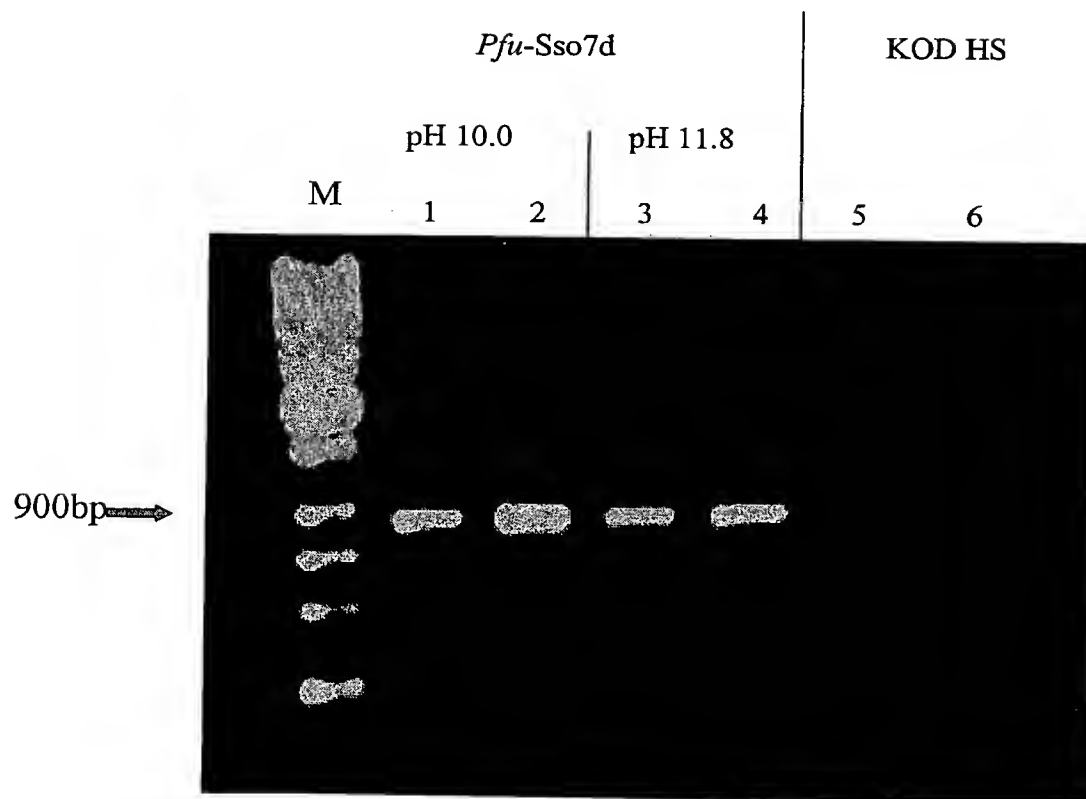


FIGURE 7

2.6kb H α AT
2''/kb - 5'' extension

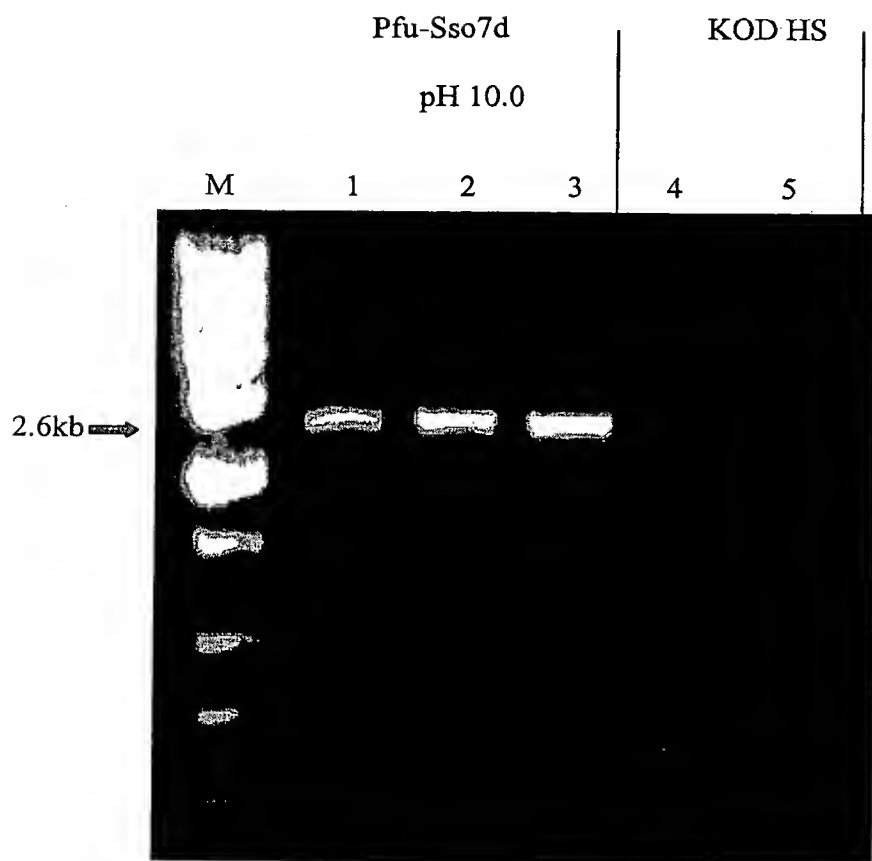


FIGURE 8

6kb BG
10"/kb - 1' extension

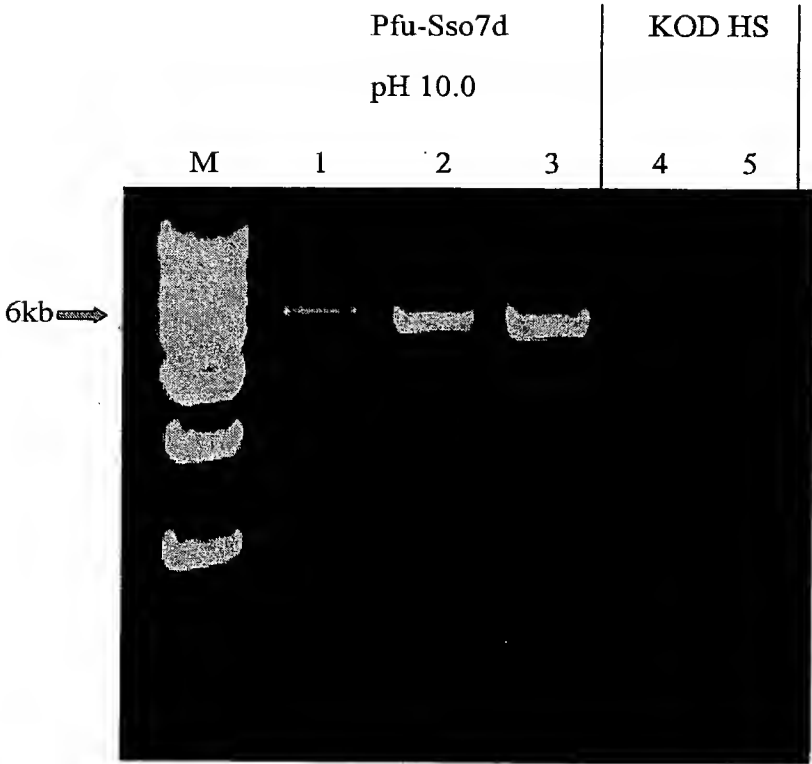


FIGURE 9

2.6kb H α AT
30''/kb - 1'. 18'' extension

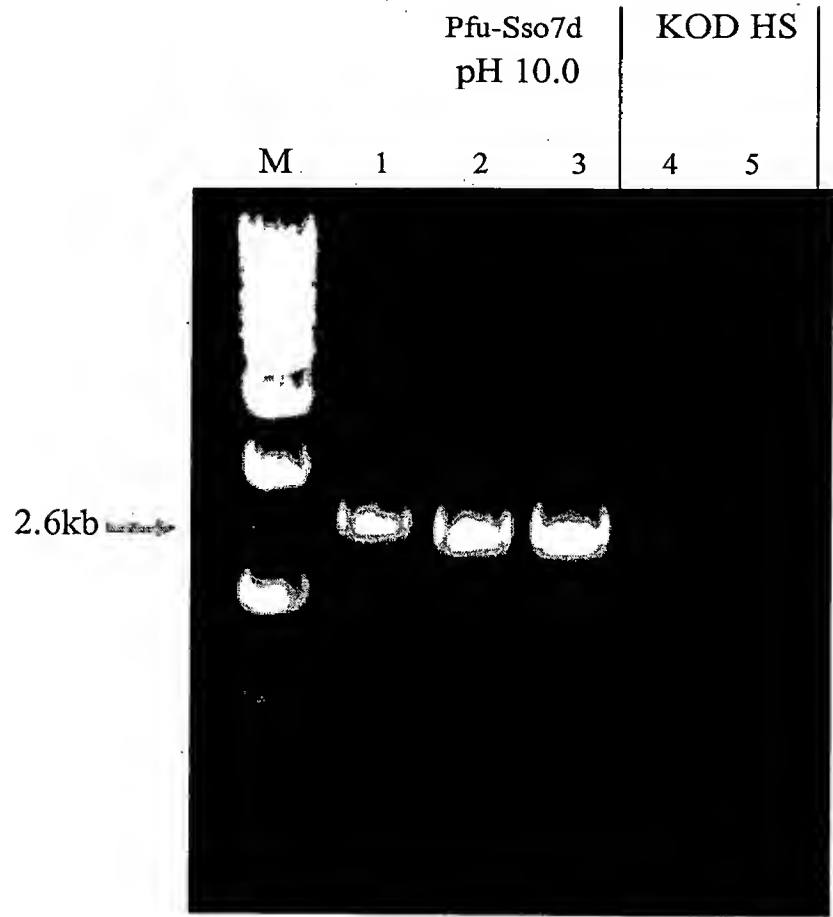


FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAGATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAGATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAGATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 13)

V93K#1

5'-gAACATCCCCAAGATAACCCACTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 15)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCCCCCACTATTAgAgAAAAAg-(SEQ ID NO: 16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID NO: 17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 18)

Cysteine

QCM#4 5'-(Phosphate)gAACATCCCCAAGATATACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCACCTATTAgAgAAAAAg-3' (SEQ ID NO: 20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 21)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

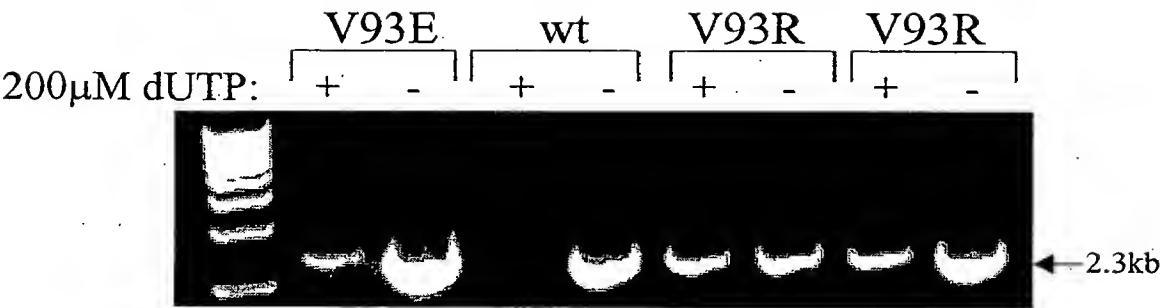
QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCCTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

FIGURE 11

a.)



b.)

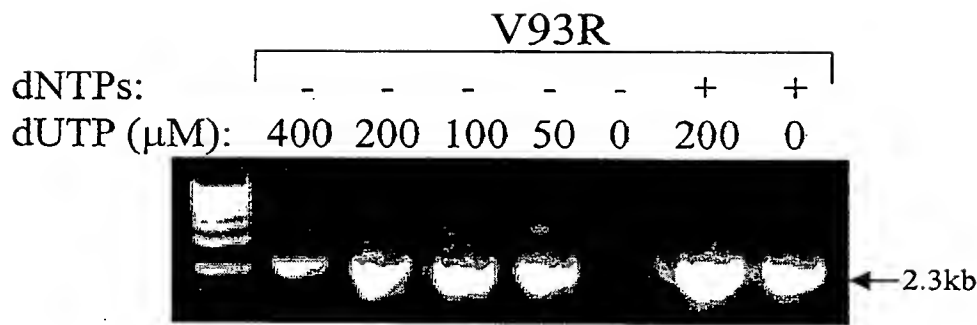


FIGURE 12

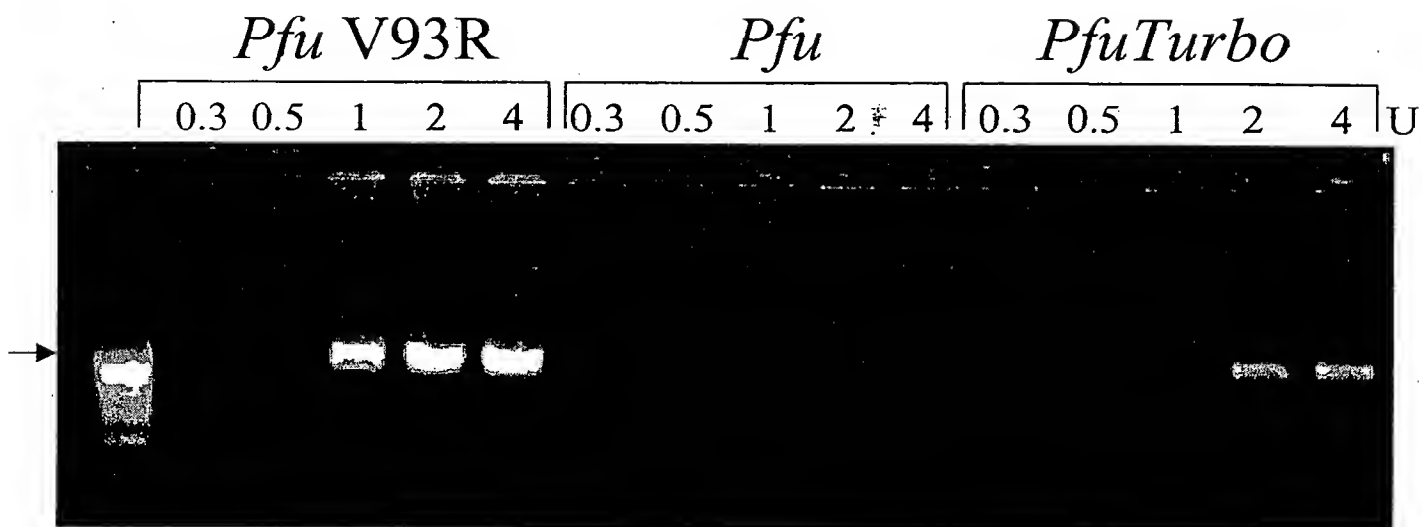


FIGURE 13A**PFU DNA POLYMERASE**

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

```
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATFCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCCTAG 2328
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FIGURE 13A (CONT.)

PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 30)

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGTTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTGCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCTTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGACTTGT 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGGTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTGA AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

```

KOD DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 33)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

```

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTAAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACNNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACCGCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCCTCAT AACCTACAAC GGCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780

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FIGURE 13A (CONT.)

TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCTTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCCG	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTTCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAAATGAGCT	GGCCCCGAAC	AAGCCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCGCGC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCGAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA		2325

Vent DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTTTAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCTCATTT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAACGTGTA	GAGTGCTCGA	TGCAGTGAAA	GTCAGGAAAA	AATTTTTTGGG	AAGGGAAGTT	240
GAACTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGACNNNC	CAGCTATGCG	GGGCAAAATA	300
AGGGAACATC	CAGCTGTGGT	TGACATTTTAC	GAATATGACA	TACCCCTTTC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCCTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	660
AAACGGGCAG	AAAAGCTGGG	AGTTCCGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAAACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGTAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAAC TTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAAC TTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAAATATCA	TTTATTTTGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
GTATCCCCAG	ATACCCTTGA	AAAAGAGGGG	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTATTCCTT	CCATAC TCGG	GGACTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTAT TAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500

FIGURE 13A (CONT.)

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GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAG 1680
AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTG TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAAATAG CAAAATACAG GGTTCCTACT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTATA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

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Deep Vent

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

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ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACNNNC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCATTCTTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGAAAAGG GACTGGAGAG AGTTGCAAAG TATTCATGAG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCA GAGCCTGTAG CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAAGTGGAG GAAAAGTTTC GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTTCGT ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220

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GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCCTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTCACGCACCCGAGGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATACCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAAACGGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACCGG
CGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCGGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTTCGCGCGCTACTCGATGGAGGACCGG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCC
CAACAAGCCCAGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTCTAGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGCCTCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCCGTTTTAAAGTCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAGTGCCTGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTGGAGGCGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGAGGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgCG
TTTGGCCGCCAGAGGTGTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTTC
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCCG
GCTTGGCGCGTGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R (SEQ ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHAPVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVRHAPVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHAPVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A (SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHAPVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/G387P (SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEMERIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKKVKYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLGLHLEERQ
KIKTKMKETQDPIEKILLDYRQAKIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTCKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A (SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEMERIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKKVKYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLGLHLEERQ
KIKTKMKETQDPIEKILLDYRQAKIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTCKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R (SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEMERIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKKVKYAEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTCKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEFDLRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E (SEQ ID NO:48)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEMERIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKKVKYAEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTCKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEFDLRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R (SEQ ID NO:49)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTRVVRVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDVVSTEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKVKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLD FRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPPEKLVIEYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

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GPILMISYADEEGARVITWKNIDL PYVDVVSTEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKVKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLD FRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPPEKLVIEYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R (SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
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GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKVKVYAEIITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLD FRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLLDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYGGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFVKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDGVEKAVRIVKEVTEKLSKYEVPPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E (SEQ ID NO:52)

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RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKVKVYAEIITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLD FRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLLDLLEERQK
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DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDGVEKAVRIVKEVTEKLSKYEVPPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI
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PKGT

>VENT V93R (SEQ ID NO:53)

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DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
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WLKR

>VENT V93E (SEQ ID NO:54)

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GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKOPDVIITYNGDNFDLPYLKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAEALAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSIILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGIFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKSGSKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R (SEQ ID NO:55)

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ILMISYADESEARVITWKKIDLPHYVEVVSTEEKEMIKRFLRVVVEKOPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKKQVYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKDFPGFIPSLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPAPERILRAFGRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E (SEQ ID NO:56)

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ILMISYADESEARVITWKKIDLPHYVEVVSTEEKEMIKRFLRVVVEKOPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKKQVYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKDFPGFIPSLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPAPERILRAFGRKEDLRYQKTRQVGLGAWLKPKGKKK

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

5'

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1 5 10 15	
agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga	96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg	
20 25 30	
aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att	144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile	
35 40 45	
gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg	192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg	
50 55 60	
gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata	240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile	
65 70 75 80	
gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc	288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile	
85 90 95	
agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac	336
Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr	
100 105 110	
gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg	384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro	
115 120 125	
atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg	432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr	
130 135 140	
ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata	480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile	
145 150 155 160	
agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc	528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile	
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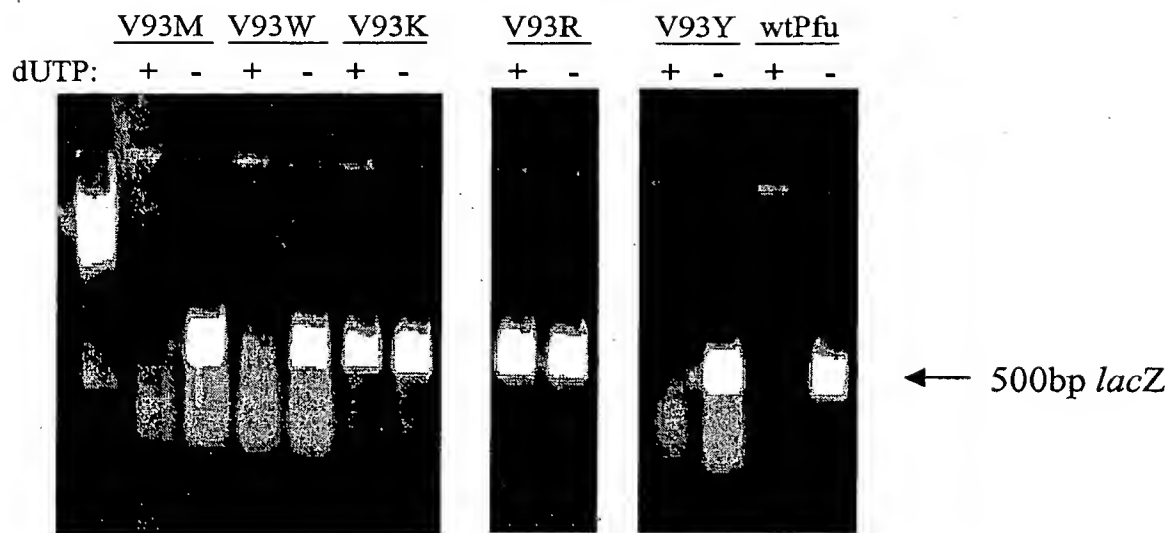
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Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	
195 200 205	
tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	
210 215 220	
aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	
225 230 235 240	
atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	
245 250 255	
cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	
260 265 270	
tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	
275 280 285	
aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	
290 295 300	
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Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr	
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Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu	
325 330 335	
gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc	1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu	
340 345 350	
gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca	1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala	
355 360 365	
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Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr	
370 375 380	
gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc	1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile	
385 390 395 400	
gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat	1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His	
405 410 415	
aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac	1296

Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Glu	Glu	Tyr	Asp	
			420					425					430			
gtg	gct	cct	cag	gta	ggc	cat	aag	ttc	tgc	aag	gac	ttc	ccc	ggc	ttc	1344
Val	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe	
			435				440					445				
atc	cca	agc	ctc	ctc	gga	gac	ctc	ttg	gag	gag	aga	cag	aag	gta	aag	1392
Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Val	Lys	
			450			455					460					
aag	aag	atg	aag	gcc	act	ata	gac	cca	atc	gag	aag	aaa	ctc	ctc	gat	1440
Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Lys	Lys	Leu	Leu	Asp	
465					470					475					480	
tac	agg	caa	cga	gca	atc	aaa	atc	ctt	gct	aat	agc	ttc	tac	ggc	tac	1488
Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	Tyr	
				485				490						495		
tac	ggc	tat	gca	aag	gcc	cgc	tgg	tac	tgc	aag	gag	tgc	gcc	gag	agc	1536
Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	Ser	
			500					505					510			
gtt	acc	gct	tgg	ggc	agg	cag	tac	atc	gag	acc	acg	ata	agg	gaa	ata	1584
Val	Thr	Ala	Trp	Gly	Arg	Gln	Tyr	Ile	Glu	Thr	Thr	Ile	Arg	Glu	Ile	
			515				520					525				
gag	gag	aaa	ttt	ggc	ttt	aaa	gtc	ctc	tac	gcg	gac	aca	gat	gga	ttt	1632
Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Phe	
			530			535					540					
ttc	gca	aca	ata	cct	gga	gcg	gac	gcc	gaa	acc	gtc	aaa	aag	aag	gca	1680
Phe	Ala	Thr	Ile	Pro	Gly	Ala	Asp	Ala	Glu	Thr	Val	Lys	Lys	Lys	Ala	
545					550				555						560	
aag	gag	ttc	ctg	gac	tac	atc	aac	gcc	aaa	ctg	ccc	ggc	ctg	ctc	gaa	1728
Lys	Glu	Phe	Leu	Asp	Tyr	Ile	Asn	Ala	Lys	Leu	Pro	Gly	Leu	Leu	Glu	
				565				570						575		
ctc	gaa	tac	gag	ggc	ttc	tac	aag	cgc	ggc	ttc	ttc	gtg	acg	aag	aag	1776
Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	Lys	
			580					585				590				
aag	tac	gcg	gtt	ata	gac	gag	gag	gac	aag	ata	acg	acg	cgc	ggg	ctt	1824
Lys	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Asp	Lys	Ile	Thr	Thr	Arg	Gly	Leu	
			595				600					605				
gaa	ata	gtt	agg	cgt	gac	tgg	agc	gag	ata	gcg	aag	gag	acg	cag	gcg	1872
Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala	
			610			615					620					
agg	gtt	ctt	gag	gcg	ata	cta	aag	cac	ggc	gac	gtt	gaa	gaa	gcg	gta	1920
Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala	Val	
625					630				635						640	
agg	att	gtc	aaa	gag	gtt	acg	gag	aag	ctg	agc	aag	tac	gag	gtt	cca	1968
Arg	Ile	Val	Lys	Glu	Val	Thr	Glu	Lys	Leu	Ser	Lys	Tyr	Glu	Val	Pro	

FIGURE 14 (CONT.)

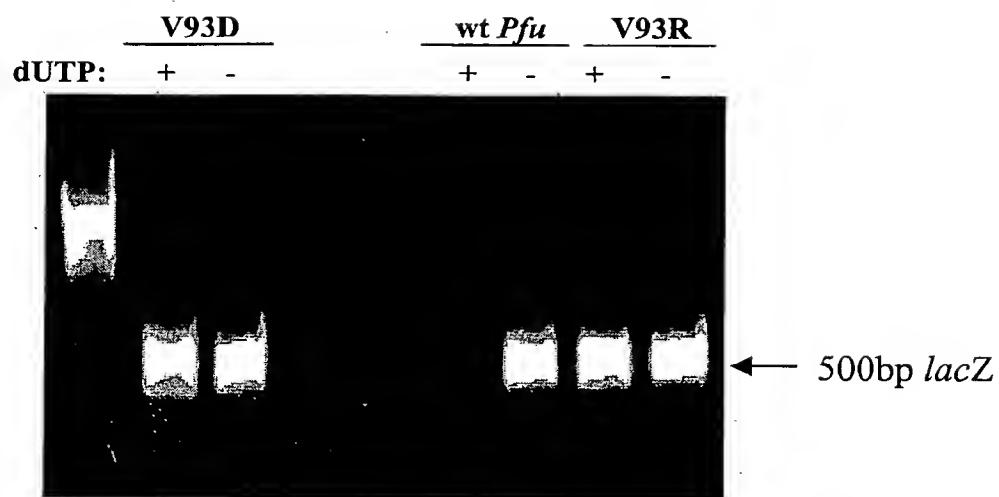
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660	665	670	
tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca			2064
Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala			
675	680	685	
agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc			2112
Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu			
690	695	700	
aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt			2160
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe			
705	710	715	720
gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag			2208
Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln			
725	730	735	
gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa			2256
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys			
740	745	750	
gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg			2304
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp			
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cta aaa cct aag aca tga			2322
Leu Lys Pro Lys Thr			

FIGURE 15A



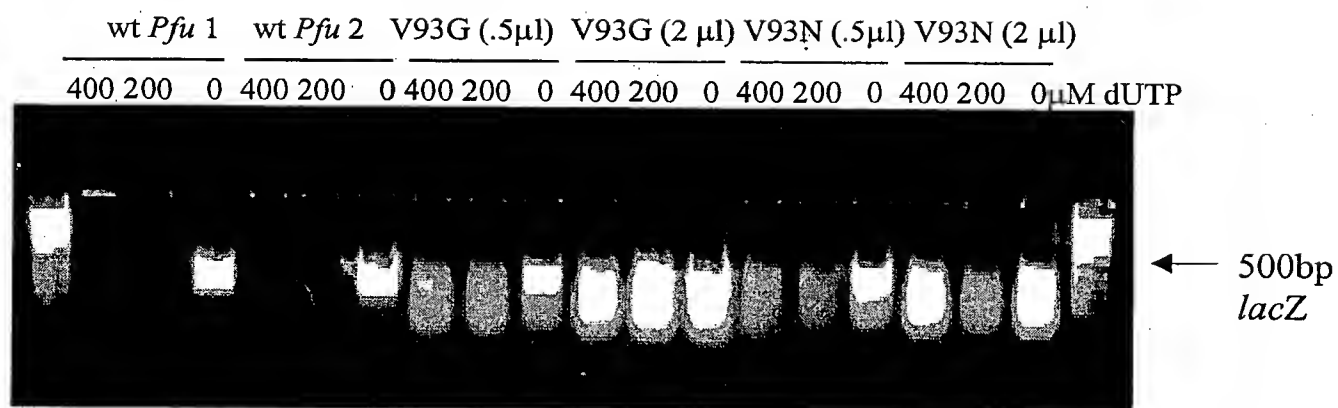
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

FIGURE 15B



Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

FIGURE 15C



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 16: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Figure 17A

Pyrococcus furiosus gene for archaeal histone (Hmf-like)
(ACCESSION No: AB013081)

Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 64)

```

M M G E L P I A P V D R L I R K A G      18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54

A Q R V S E Q A A K V L A E H L E E      36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108

K A I E I A K K A V D L A K H A G R      54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA    162

K T V K V E D I K L A I K S *      69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA      207
```

Figure 17B

(Hmf-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

```

M M G E L P I A P V D R L I R K A G      18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54

A Q R V S E Q A A K V L A E H L E E      36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108

K A I E I A K K A V D L A K H A G R      54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA    162

K T V K V E D I K L A I K S      69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC
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FIGURE 17B (CONT.)

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      G   G   G
    // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG CTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

```

FIGURE 17B (CONT.)

A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGC TAC GGC

 G E W T E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

FIGURE 17B (CONT.)

A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT
 H H *
 CAT CAT TAA

Figure 17C**Taq DNA polymerase-(Hmf-like) fusion protein**

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

G G G
 GGC GGC GGT

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

FIGURE 17C (CONT.)

D G H H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACG CCA

 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG

 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GGC AGC CTG

 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L

FIGURE 17C (CONT.)

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGC CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

FIGURE 17C (CONT.)

G K T E K T G K R S T S A A V L E A
 GGC AAG ACG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC AGC GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

FIGURE 17C (CONT.)

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT

H H //
CAT CAT //

M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17D

Pfu DNA Polymerase (WT) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

FIGURE 17D (CONT.)

//

ccctggctct gggctccacat atatgtttctt actcgcccttt atgaagaatc ccccgatcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattttctat
caactctaca cctccccctat ttctctctctt atgagattttt taagtatatgt tatagagaag
gtttttact ccaaaactgag ttagtagata tgtgggggagc ataatgatttt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctctttctca gggatgatcc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aagggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaactttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttogaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctctta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gattttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaatttt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

ccctccaatg gaaattcagc ttccaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggtcaggg agagctacac
aggtggattc gttaaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctgggttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaatactc cttgactata gacaaaaagc
gataaaaact ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggctctta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggttta gagatagta ggagagatg gagtgaaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaaga
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccagggttct ccagcggtag ttaggatatt

FIGURE 17D (CONT.)

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ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taactttttac agaaaataact gtctcaaat atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaatttt tcttttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnnga
aagattgaga tgttcttg //
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```


Figure 17E

(Hmf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggtcct ggggtccacat atatgttctt actcgccctt atgaagaatc ccccgatcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgatcc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggaagcct attaccgtgt ggaacttta
tttggaaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

tcgtgggtta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtcgcct
acaattttttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccggggagt ttgtgattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taactttttac agaaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

FIGURE 17E (CONT.)

cgagagagag atgataaaga gattttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaacccttga
gagagttgcc aaataactga tggaagatgc aaaggcaact tatgaactcg ggaaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgttttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggctcaggg agagctacac
aggtaggattc gttaaagagc cagaaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgggttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaaatt ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggattttaa agtcctctac attgacactg atgggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac

FIGURE 17E (CONT.)

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
 ctcgatttcc ttggttgtgc tccatatgat aagctttccaa agtgggtgtt cagactttta
 gacactcaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
 gtagaagcgg cactactcag atgttcccc aggaatgagg ttgtgttagc tcntcccnga
 aagattgaga tgttcttgg // TGA

Figure 17F**(Hmf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein**

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
 AAAAGGGCAG AAAAACITGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

FIGURE 17F (CONT.)

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTAGGGAGA GTATACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TACTATTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTAATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCITTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC // 2328
// TGA

Figure 17G

PFU DNA POLYMERASE (V93 R OR E) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

FIGURE 17G (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTATCTGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GATTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
 AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCNACTTAT 960
 GAACCTCGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAT AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAATGCTG GGAAGAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GATGCTAGA GCTTGAATAT 1740
 GAAGGTTTTT ATAAGAGGGG ATTCCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTATAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAAT 2100
 GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220

FIGURE 17G (CONT.)

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GGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) - (HMF-like) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAAGC GAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXX CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCGAG AAAAAGTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCT CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGTGA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTTGAGAG ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGTTCTTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAAGAGGAGTA TCAAAGAAGG 1140

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FIGURE 17H (CONT.)

CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATT TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACAT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GAGAGGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG AAGCTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGATAG TAAAGNAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAAGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGACAA GTATGACGCA GAATATTACA TCGAGAACCA GGTCTTTCCA 2220
GCGTACTTGA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAACAAAG TCGGCCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTT GCA ATT AAG AGC TGA

Figure 17I

(HMF-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATT TTGGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
 AGAGACATCA CAGCGTTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITGCCCTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTTACTTGA AAAACATAGA TCITCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTTAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
 AAAAGGGCAG AAAAACTTGG GATTAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAAATACA TTTCCACTTG 780
 TATCATGTAA TAACAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGT GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACTTAT 960
 GAACTCGGA AAGAAATCCT TCCAATGGAA ATTACGCTTT CAAGATTAGT TGGACAACT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTTGAG AGTGTTCTT ACTTAGGAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGAGTA TCAAGAGAG 1140
 CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGSGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGAATA TAATTACCCA CAATGTTTCT 1260
 CCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAATGCCCTG GGGAAAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAAGT AATACAAAAAG CTTGCCAATT ATGAATTTCC ACCAGAGAAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAAGGCGAT AGGTCTCAC 2040
 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAAATATTACA TGGAGAAACCA GGTCTTCCA 2220

FIGURE 17I (CONT.)

GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17J**(HMF-LIKE) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein**

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXX CCACATATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITTGCCCTC 420
 GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCTTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGGCAG AAAACCTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAITCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

FIGURE 17J (CONT.)

TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GGT₌GGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACATAGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCCTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17K

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240

ACCGTGTGGA	AAC ^T TTATATT	GGAACATCCC	CAAGATYXXK	CAC ^T ATTAG	AGAAAAGTT	300
AGAGAACA ^T C	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTGC	AAAGAGATAC	360
CTCATCGACA	AAGGCC ^T TAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TC ^T TGCCTTC	420
<u>GCN</u> ATAGCNA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTTGGA	AAAACATAGA	TC ^T TCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCC ^T G	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTC ^{CC}	ATATTTAGCG	660
AAAAGGGCAG	AAAAA ^C TTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTTCGACTTG	780
TATCATGTAA	TAAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTAATAGAA	840
GCAATTTTTG	GAAAGCC ^{CA} AA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGC ^{AA}	GGCACTTAT	960
GAAC ^T CGGGA	AAGAAATCC ^T	TCCAATGGAA	ATTCAAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTTCAAGGTG	AAGCACAGGG	AACCTTGTATG	AGTGGTTCTT	ACTTAGAGAA	1080
GCCTACGAA ^A	GAACGAA ^T G	AGCTCCAAAC	AAGCCAAGTG	AAGAGAGTA	TCAAAAGAA ^G	1140
CTCAGGGAGA	GCTACACA	GGTGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACC ^{CA}	CAATGTTTTCT	1260
CCCGATAC ^{TC}	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAAC ^T CTTA	GCAAATCTTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCC	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCCTAGAA ^T	TTGTAAAATA	CATAAATTC ^A	AAGCTCCCTG	GACTGCTAGA	GC ^T TTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAAC	ACGGAGATGT	TGAAGAAAGCT	1920
GTGAGAATAG	TAAAAAGAA ^{GT}	AATACAAAAAG	CTTGCCAATT	ATGAAAATTC	ACCAGAGAAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGTCTCTCAC	2040
GTAGCTGTTG	CAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGTTAATT	2100
GGATCATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTAGGAA	2160
TACGATCCCC	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTGGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCTCTGGCTT	AACATTAAAA	AATCC //		2328
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GGT						
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA						
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA						
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA						

Figure 17L

KOD DNA POLYMERASE - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACCTGACTA CATAACCGAG GATGAAAGC CTGTCAATAG AATTTC AAG 60
AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCTTAC 540
GTTGACGTGC TCTCGACCGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GGCAGCAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAA 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AATAAACCA AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCAATAC 960
GAGCTTGGGA AGGATTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAGGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGAGA GGGCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680

FIGURE 17L (CONT.)

```
ATGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGGCTT CTTGCTCAGC AAGAAGAAGT ATGCGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGTTTCT TGAAGCTTTG CTAAGAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGAATTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCATTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCTGTC TCAAGGGCTC TGGGAGGATA GGCACACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
//
    ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
    GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
    AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
    AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17M

(Hmf-like) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
```

```
ATGATCTCG ACACGTGACTA CATAACCGAG GATGGAAGC CTGTCTATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCAGCAGG AGCTGAAAAT GCTCGCCTTC 420
```

FIGURE 17M (CONT.)

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
 GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGGACAACT TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTACAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGA 900
 ACGGGCGAGA ACGTTCGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
 CAGCTGGGA AGGATTTCTT TCCGATGGAG GCCACGTTT CTCGCTTAAT CGGCCAGTCC 1020
 TCTCTGGAG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTCTT CTTAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGT GGCAGAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
 AGGGCGCGT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGG AAGGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGGC CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCTGTCAG AAGAAGAAGT ATGCGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCG ACITGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGGAITTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCACAGAGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCTGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17N**(Hmf-like)-Vent DNA POLYMERASE FUSION PROTEIN**

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

FIGURE 17N. (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) ;

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //	

ATGATACTGG AACTGATTA CATAACAAAA GATGCAAGC CTATAATCCG AATTTTAAAG	60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT	120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCA TAAAGGGCGA GAGACATGGA	180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAAGGAAAA AATTTTGGG AAGGGAAGTT	240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA	300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT	360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CTTGCGCTTT	420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT	480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT	540
GTGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA	600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAAAT TTGATTTGCC GTATCTATA	660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA	720
CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGGAAG TCAAGGGTAG AATCCACTTT	780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT	840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA	900
TGGGAACACG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA	960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT	1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA	1080
AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA	1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAGA AGCCAGAAAA AGGTTTGTGG	1200
GAATAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAA	1260
GTATCCCCAG ATACCTTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA	1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTTCCCT CCATCTCGG GGACTTAAT	1380
GCAATGAGGC ATAGATATAA GAAGAAAATG AATCCACAA TTGACCCGAT CGAAAAGAAA	1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG	1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG	1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGCTT TAAGGTTCTT	1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATATAA	1680
AAGAAAGCCA AGGAATTCCT AAACATACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT	1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA	1800
GATGAAGAGG GCAGGATAAC AACNAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG	1860

FIGURE 17N (CONT.)

ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTTCACATT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGTT AATTTTACTT 2160
ACAGAAATACG ATCTTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTAAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17O

Vent DNA POLYMERASE - (Hmf-like) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAATA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCATTT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGGTTTGTGG 1200

FIGURE 170 (CONT.)

GAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTACAAC 1260

GTATCCCCAG ATACCTTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320

GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTAATT 1380

GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAGAAA 1440

ATGCTCGATT ATAGGCAAG GGCATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500

GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560

AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGGCTT TAAGGTTCTT 1620

TATGCGGACA CTGACGGCTT TTA TGCCACA ATACCCGGG AAAAGCCTGA ACTCATTAA 1680

AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740

GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800

GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860

ATAGCTAAGG AGACTCAGGC AAAGTTTGA AGGCTATAC TTAAGAGAGG AAGTGTGAA 1920

AAAAGCTTG TTAATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 1980

CCTCATGTCG CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2040

ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGT AATTTTACTT 2100

ACAGAATACG ATCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2160

TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2220

CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17P

Deep Vent- (Hmf-like) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60

AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120

CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGG 180

AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGG GAGGCCGATT 240

GAGGTATGGA GGCCTGACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300

AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360

FIGURE 17P (CONT.)

CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420												
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480												
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCCTCCCGTAC	540												
GTCAGGAGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600												
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660												
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720												
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780												
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840												
GCAATCTTCG	GAAGCCCAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900												
ACTGGAAGG	GACTGGAGAG	AGTTGCAAG	TATTCAATGG	AGGATGCAAA	GGTAAACGTAC	960												
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020												
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080												
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140												
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200												
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260												
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320												
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380												
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440												
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500												
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560												
TATATAGAGT	TCGTAAGGAA	GGAAC TGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620												
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680												
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740												
GAGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800												
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860												
AAAGAAACCC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920												
GTAAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980												
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040												
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100												
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160												
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220												
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280												
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328												
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

FIGURE 17Q

(EMflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA	
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	180
AAGATGTGA GAATTATAGA TGCCGAAAGA GTTCCCTGGG GAGGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCTT CAGGACXXXC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC	360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGATGAAG AGCTCAAGTT GCTCGCATTT	420
GACATAGAAA CCTCTATCA CGAAGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGGAG	900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTTCAATGG AGGATGCAAA GGTAACTAC	960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC	1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG	1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG	1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG	1200
TTAGTTTCCC TAGATTTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA	1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC	1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA	1380
AGGCAAGTAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT	1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTTATGGTA TTATGGGTAC	1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA	1560

FIGURE 17Q (CONT.)

TATATAGAGT	TCGTAAGGAA	GGAAGTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GGTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GTTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGCTATCTCT	TGCAGAGGAG	2160
TTTCGATCTCA	GGAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAAGGTGAAGAAAAGTTCCTCGG
CAGGTCTGTGGAGGTCGTGGTCCCTCTACTTCACGCACCCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGGTCAATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGGAGATCGAGCGCTTACCCAGGGAGAGAGTTCGGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTTGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAGGAGATGATTAA
GCGCTTCTTGAGGGTCGTTAAGGAGAGGACCCGACGTGCTGATAACATACACCGCGCAACTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAGCTTGCGGTGAGCTTT
ACCTTCGGAGGGA CGGGAGCGAGCCGAAGATA CAGCGCATGGGGACAGGTTTGCGGTGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACATAA
ACCTCCGACCTACACCTTGAGGTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGGCGCTACTCGATGGAGGACGCGAGGGTTACTACGAGCTTGGCAGGAGTTCCTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGCTCCAGCACCCGGCAACCTCGTCGATGGTTCCTCTTAAGGAAGGCTTACGAGAGGAACGAATCGCTCCCAACAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGCGGTGGCTACGTCAAGGACCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTTA~~CCCT~~CAATCAATAATCA~~CC~~CAACAGTCTCGCCAGATAC
GCTCAACCGCGAGGGGTGATGAGACTACGAGCTTGGCCCGAGGTGGTCA CAAGTTCTCAAGGACTTCCCGGCTTCATCCGAGCCCTGTCGAAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCTCGATTACAGGCAACG~~CCG~~ATCAAGATTCTCGCCAAACAGTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCGAGGAGTGGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAGATTTCGGTTTAAAGTCTC
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGGGGCTTCTTCGTCA CGAAGAAAAAGTACGCGGTCTATCGACGAGGAGGGCAAGATAACCA CGCGCGGGCTTGAGATAGTACGAGCGG

ACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTTGAAGAGGCCGTGAGAAATTGTACAGGAAGTCAACGAAAGCTGAGCAA
 GTACGAGGTTCCGCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAGGCCACCGGCCCGCAGTAGCCATAGCGAAGcGTTTGGCCCGCAGAGGT
 GTTAAATCCGCGCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATG
 CGGACTACTACATCGAGAACCAGGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTCGGCTACCAGAAGACGAGGCGAGTCTGGGCTTGGCGC
 GTGGCTGAAGCCGAAGGGAAGAAG//

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17S

(Hmf-like) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	//				

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC
 CTACTTCTACGCGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAAGGTGA
 AGAAAAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGTCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGGTCATC
 GACATCTACGAGTACGACATACCTTCGCCAAGCGCTACTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACGATCGA
 GACGCTCTACCACGAGGAGAGAGTTTGGAAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTTGAAGAAAGATCGACCTTC
 CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAAGCGTCTTTGAGGGTCTGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACAACGGCGACAACCTTC
 GACTTCGCTTACCTGAAAAAGCGTGTGAGAAGCTTTGGCGTAGCTTTACCTCGGAGGAGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGGT
 CGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC
 CCAAGGAGAAGGTTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAGGTCGCGCGTACTCGATGGAGGACCGAGGGTTACCTACGAG
 CTTGGCAGGGAGTTCTTCCGATGGAGGCCACGTTTCCAGGCTCATCGGCCAAGCCCTCTGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTT
 CCTAAGGAAGGCCCTACGAGAGGAACGAACTCGCTCCCAACAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGTACgCCGTGGCTACGTCGAGGAGCCGG
 AGCGGGGACTGTGGGACAAATATCGTGTAATCTAGACTTTCTAGTCTCTA[CC]TCAATCAATAACCCACAACGTCCTGCCAGATACGTCACCCGAGGGGTGT
 AGGAGCTACGACGTTGGCCCCCGAGGTCGATCAAGTTCTGCAAGGACTTCCCCGGCTTCATTCGAGGCCTGCTCGGAAACCTGCTGGAGGAAGGCGAGAATAAA

FIGURE 17S (CONT.)

GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGGCCATCAAGATTCTCGCCAAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTTAA
GTCCTCTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAAT
GCCCCGCCCTTCTCGAACTCGAATACGAGGGCTTCTAAGTCAGGGGCTTCTTCGTACGAAGAAAAAGTACGCCGTCTCGACGAGGAGGCAAGATAACCCACGCGCG
GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGTTTGGAGGCGGATACCTCAGGCCACGGTGA CGTTGAAGAGGCCCGTCAGAATT
GTCAGGGAAGTCAACCGAAAAAGCTGAGCAAGTACGAGGTTCCGCCGAGAAAGCTGGTTATCCACGAGCAGATAACGCCGCGAGCTCAAGGACTACAAGGCCACCGGCC
GCACGTAGCCATAGCGAAGCGTTTGGCCGCCAGAGGTGTTAAAAATCCGGCCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG
CGATTCCCTTCGACGAGTTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCCTCAGGGGCCCTTCGGC
TACCGCAAGGAAGACCTGCGCTAC CAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archaeal histone (Hmf-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082)
/product="pcna sliding clamp (proliferating-cell nuclear antigen) "

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162

FIGURE 17T (CONT.)

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GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
E F I M K A E G E T Q E V E I K L T 180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540

L E D E G L L D I E V Q E E T K S A 198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594

Y G V S Y L S D M V K G L G K A D E 216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648

V T I K F G N E M P M Q M E Y Y I R 234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702

D E G R L T F L L A P R V E E * 250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA 750

```

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

```

M P F E I V F E G A K E F A Q L I D 18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54

T A S K L I D E A A F K V T E D G I 36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108

S M R A M D P S R V V L I D L N L P 54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162

```

FIGURE 17U (CONT.)

S S I F S K Y E V V E P E T I G V N	72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
M D H L K K I L K R G K A K D T L I	90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
L K K G E E N F L E I T I Q G T A T	108
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
R T F R V P L I D V E E M E V D L P	126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
E L P F T A K V V V L G E V L K D A	144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
V K D A S L V S D S I K F I A R E N	162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
E F I M K A E G E T Q E V E I K L T	180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
L E D E G L L D I E V Q E E T K S A	198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
Y G V S Y L S D M V K G L G K A D E	216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
V T I K F G N E M P M Q M E Y Y I R	234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
D E G R L T F L L A P R V E E	250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG	
G G G	
// GGC GGC GGT	
V T S G M L P L F E P K G R V L L V	

FIGURE 17U (CONT.)

GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG
 D G H H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
 S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG CCC ACG CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTC GGC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

REPLACEMENT SHEET

FIGURE 17U (CONT.)

A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

 G E W T E E A G E R A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

FIGURE 17U (CONT.)

A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P

REPLACEMENT SHEET

FIGURE 17U (CONT.)

```

ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT
H H *
CAT CAT TAA

```

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

FIGURE 17V (CONT.)

Nucleotide sequence (SEQ ID NO: 65) /Nucleotide sequence (SEQ ID NO: 67)
 Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

G G G
 // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

REPLACEMENT SHEET

FIGURE 17V (CONT.)

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G G GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
CTG GCC GCC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GGC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

REPLACEMENT SHEET

FIGURE 17V (CONT.)

A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT
S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F

REPLACEMENT SHEET

FIGURE 17V (CONT.)

CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCC GGC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT
H H //
CAT CAT //

REPLACEMENT SHEET

FIGURE 17V (CONT.)

M P F E I V F E G A K E F A Q L I D	18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
T A S K L I D E A A F K V T E D G I	36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
S M R A M D P S R V V L I D L N L P	54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
S S I F S K Y E V V E P E T I G V N	72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
M D H L K K I L K R G K A K D T L I	90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
L K K G E E N F L E I T I Q G T A T	108
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
R T F R V P L I D V E E M E V D L P	126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
E L P F T A K V V V L G E V L K D A	144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
V K D A S L V S D S I K F I A R E N	162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
E F I M K A E G E T Q E V E I K L T	180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
L E D E G L L D I E V Q E E T K S A	198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
Y G V S Y L S D M V K G L G K A D E	216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648

FIGURE 17V (CONT.)

V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17W**Pfu DNA Polymerase (WT) -(PCNA) fusion protein**

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

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ccctggtcct gggtcacat atatgttctt actgcctttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat gaaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggaagcct attaccgtgt gaaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct

```

FIGURE 17W (CONT.)

aataccaatg gagggggaag aagagctaaa gattcttgcc ttogatatag aaacctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaataactga tggaaagatgc aaaggcaact tatgaactcg ggaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggctcaggg agagctacac
agggtggattc gttaaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttagactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta

FIGURE 17W (CONT.)

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agagggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaaagcc aggaatggta attggataca tagtactttag
aggcgatggg ccaattagca ataggggcaat tctagctgag gaatacgcgc ccaaaaagca
caagtatgac gcagaatatc acattgagaa ccagggttctt ccagcgggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaacttga cttctacaac atttctaact ttgcaactct

REPLACEMENT SHEET

FIGURE 17W (CONT.)

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgacgac gtagatcttt
 ttgtctcaa gcagagccgc tccaatggat aacacccttg ttcccgacc caagtccgct
 acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
 ttccgggagt tttgtattgc tctagccaag gtttgggatt tttagaatcct ttaactctgg
 aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
 taacttttac agaaaataact gtctcaaaatt atgacaaactc ttgacatttt tacttcat
 ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
 ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
 gacactcaaa taccagacga caatggtgtg ctactcaag ccccatatgg gttgagaaaa
 gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntccnga
 aagattgaga tgttcttg //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GCA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA TAT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG
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ccctggtcct ggggccacat atatgttctt actcgccctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gtttttact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtatttc aaaaaagaga acggaataatt
```


FIGURE 17X (CONT.)

taagatagag catgatagaa cttttagacc atacatttac gctctttctca gggatgattc
aaagattgaa gaagttaaga aaataaacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggcaagcct attaccgtgt ggaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatcg atattccatt tgcaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaaa gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gattttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaaagatgc aaaggcaact tatgaactcg ggaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgttt ctacttagg aaagcctacg aaagaaacga
agtagctcca acaaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac
aggtggattc gttaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt

FIGURE 17X (CONT.)

tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaatgaag gaaactcaag atcctataga aaaaatactc ctigactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttta agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaaggaa aagtcattac
tcgttggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agtttttgag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaaga
actagctgct aaaggagtta aaataaaagcc aggaatggta attggatata tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcttg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt

REPLACEMENT SHEET

FIGURE 17X (CONT.)

tctaacccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
 tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
 ttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggg
 ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
 cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
 tcaagatttt ctaaaagaat tttaacggcc tctctgtcaa ttctgacgac gtagatcttt
 ttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
 acaatttttt ccttgatatc cctaattgtat aagcaagcca aggagagta gatgctacct
 ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
 aaagtataat ttcaagctcc ttctttctca tgacagatga aaaattgttt tgtctctttt
 taacttttac agaaataaact gtctcaaaat atgacaaactc ttgacatttt tacttcatta
 ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtcctctc
 ctcgatttcc ttgggttgtc tccatatgat aagcttccaa agtgggtgtt cagactttta
 gacactcaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
 gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnga
 aagattgaga tgttcttg // TGA

FIGURE 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 67) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGG ATGATTTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAA GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGAT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600

FIGURE 17Y (CONT.)

AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCAATCCC ATATTTAGCG 660
AAAAGGCGAG AAAAACCCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGTACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAAGGAGTG GCTGAGAGCG TTACTGCGCTG GGAAGAGAA 1560
TACATCGAGT TAGTATGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATG AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGGCCAAAT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
// TGA

Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) -(PCNA) fusion protein

FIGURE 17Z (CONT.)

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)
 Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCCTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGCGAG AAAAACTTGG GATTAAATTA ACCATTGGA AGATGGAAG CGAGCCCAAG 720
 ATGACAGAAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAAGTC AAGCACAGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTCG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCCTATGTC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800

FIGURE 17Z (CONT.)

GAAGGAAAAG	TCATTACTCG	TGGTTTtagag	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860			
AAAGAAATC	AAGCTAGAGT	TTTTGGAGACA	ATACTAAAAAC	ACGGAGATGT	TGAAGAAGCT	1920			
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCCAATT	ATGAAATTCC	ACCAGAGAAG	1980			
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGTCCCTCAC	2040			
GTAGCTGTTG	CAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100			
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160			
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTCTTCCA	2220			
GCGGTACTTA	GGATATTGGA	GGGATTGGGA	TACAGAAAAG	AAGACCTCAG	ATACCAAAAG	2280			
ACAAGACAAG	TCGGCCTAAC	TTCTGGGCTT	AACATTAAAA	AATCC //		2328			
ATG CCA	TTT GAA	ATC GTA	TTTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAT	GAG GCC	GCG TTT	AAA GTT	ACA GAA	GAT GGG	ATA 108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GAT	GTT GTC	CTG ATT	GAC CTA	AAT CTC	CCG 162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GAA CCA	GAA ACA	ATT GGA	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA	GGA ACT	GCA ACA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	CTT GGA	GAA GTC	CTA AAA	GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAT	GAA GAT	GAG ATA	AAG CTA	ACT 540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	TTT AAA	GGA CTT	GGA AAG	GCC GAT	GAA 648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17AA (CONT.)

G387p Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG	ATGTGGATTA	CATAACTGAA	GAAGGAAAAAC	CTGTATTATTAG	GCTATTCAAA	60
AAAGAGAACG	GAAAATTTAA	GATAGAGCAT	GATAGAACTTT	TTAGACCATA	CAATTACGCT	120
CTTCTCAGGG	ATGATTCAAA	GATTGAAGAA	GTTAAGAAAA	TAACGGGGGA	AAGGCATGGA	180
AAGATTGTGA	GAATTGTTGA	TGTAGAGAAG	GTTGAGAAAA	AGTTTCTCGG	CAAGCCTATT	240
ACCGTGTGGA	AACTTTATTT	GGAAACATCCC	CAAGATXXXC	CCACTATTAG	AGAAAAAGTT	300
AGAGAACATC	CAGCAGTTGT	GGACATCTTC	GAATACGATA	TTCCATTTCG	AAAGAGATAC	360
CTCATCGACA	AAGGCCCTAAT	ACCAATGGAG	GGGGAAGAAG	AGCTAAAGAT	TCTTGCCCTTC	420
GATATAGAAA	CCCTCTATCA	CGAAGGAGAA	GAGTTTGGAA	AAGGCCCAAT	TATAATGATT	480
AGTTATGCAG	ATGAAAATGA	AGCAAAAGTG	ATTACTTTGA	AAAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	660
AAAAGGGCAG	AAAACTTTGG	GATTAAATTA	ACCATTTGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAAACAAGGAC	AATAAATCTC	CCAACATACA	CACATAGAGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAA	GGCAACTTAT	960
GAACTCGGGA	AAGAAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTAG	AGTGTTCCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAAT	AGCTCCAAAC	AAGCCAAAGT	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACACC	NGGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAAC	1200
ATAGTATACC	TAGATTTTAT	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATACTC	TAAATCTTGA	GGGATGCAAG	AACATATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAACCTTTA	GCAAATTCIT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCCTG	GGGAAGAAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GAITTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACATATCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAAATCA	AAGCTCCCTG	GACTGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAAC	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCCAATT	ATGAAATTC	ACCAGAGAAG	1980

FIGURE 17AA (CONT.)

CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17BB (CONT.)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GAT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GAT GAT GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAT GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GAA GAG //	
ATGATTTTAG ATGTGGAATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA	60
AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT	120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA	180
AAGATTGTA GAAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT	240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT	300
AGAGACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC	360
CTCATCGACA AAGGCCATAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITGCTTC	420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT	480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITCCATAC	540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG	600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG	660
AAAAGGCGAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG	720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG	780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA	840
GCAATTTTGA GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGAA	900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACTTAT	960
GAACTCGGA AAGAAATTCCT TCCAATGGA ATTTCAGCTTT CAAGATTAGT TGGACAACCT	1020
TTATGGGATG TTTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACITTAGGAA	1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG	1140
CTCAGGGAGA GCTACACACC NGGAATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC	1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAAATTACCA CAATGTTTCT	1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC	1320

FIGURE 17BB (CONT.)

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AAGTTCCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAGAA 1560
TACATCGAGT TAGTATGGA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAITCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC //TAG 2328

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Figure 17CC

(PCNA) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216

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FIGURE 17CC (CONT.)

ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA	60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT	120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCAATGA	180
AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAAA AGTTCTCTCG CAAGCCTATT	240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT	300
AGAGAACATC CAGCAGTTGT GGACATCTTC GNAATACGATA TTCCATTTCG AAAGAGATAC	360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAA AGCTAAAGAT TCITGCCCTC	420
GCAATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT	480
AGTTATGCAG ATGAAAATGA AGCAAAGTG ATTACTTGA AAAACATAGA TCITCCATAC	540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAT TTCTCAGGAT TATCAGGGAG	600
AAGGATCCTG ACATTATAGT TACTTTAAT GGAGACTCAT TCGCAITCCC ATATTTAGCG	660
AAAAGGGCAG AAAACITGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG	720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG	780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA	840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGAA	900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT	960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT	1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA	1080
GCCTACGAAA GAAACGAAGT AGTCCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG	1140
CTCAGGGAGA GCTACACA GTT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC	1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT	1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC	1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA	1380
AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT	1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT	1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGAAGAAAG	1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT	1620

FIGURE 17CC (CONT.)

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GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGRAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCATATTCT AGCTGAGGAA 2160
TAGCATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCITTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
TGA

```

Figure 17DD

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATGATTTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTTGA AACTTTATTT GGAACATCC CAAGATXXX CCACTATTAG AGAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGATATAC 360
CTCATGCACA AAGGCCCTAAT ACCAATGGAG GGGGAGAAG AGCTAAAGAT TCTTGCCTTC 420
GGNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480

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FIGURE 17DD (CONT.)

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AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
AAAAGGGCAG AAAAACITGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGAGAGGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCNACTTAT 960
GAATCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACATATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCGTGA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAITCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCCTATGTC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGNAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCTGTCCTT AACATTAAAA AATCC // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324

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FIGURE 17DD (CONT.)

AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACACGTGACTA CATAACCGAG GATGGAAAGC CTGTATAAG AATTTCAAG 60

AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120

CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180

ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240

GAGGTCCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCITCGC CAAGCGCTAC 360

CTCATAGACA AGGGATTAGT GCCAATGGAA GGCAGACGAGG AGCTGAAAAT GCTCGCCTTC 420

GACATTGAAA CTCCTTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CTTATGATA 480

AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCTAC 540

GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600

AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCACAACT TCGACTTCGC CTATCTGAAA 660

AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720

ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780

TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840

GCCGTCCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900

ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTCACATAC 960

FIGURE 17EE (CONT.)

GAGCTTGGGA	AGGAGTTCT	TCCGATGGAG	GCCCAGCTTT	CTCGTTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGTC	CAGCACTGGC	AACCTCGTTG	AGTGTTTCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGGAAG	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCCTGGG	AAGGAGTAC	1560
ATAACGATG	CAATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGGCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAAGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAAG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAATTAC	CGAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCTGTG	TCAAGGGCTC	TGGAGGATA	GCGCAGAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAAGT	TCTCCAGGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CT	2325	
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54					
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108					
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTA GAT GAC CTA AAT CTC CCG	162					
TCA AGC ATA TTT AGC AAA TAT GAA TAT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216					
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270					
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324					
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378					
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432					
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486					
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540					
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594					
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648					
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702					
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA						

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAGC CTGTACATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
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FIGURE 17Ff (CONT.)

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGG AGAACGTGGA AGAACCTTAC 540
 GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGGACAACT TCGACTTCGC CTATCTGAAA 660
 AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTACAGAGG TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAAGGT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
 CTCTGGAGG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CTTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
 ATAAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGGC CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGGCTT CTTCTGTCAG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTGCA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
 GCCGTGCGCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

FIGURE 17GG

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

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ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCAAT TTCAGCCCTA TATATAIGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720

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FIGURE 17GG (CONT.)

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CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTtaggAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTGTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTCG TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG TAG 2325

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Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN

FIGURE 17HH (CONT.)

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTTCATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGTCAATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGCCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCCTT 420
 GATATTGAAA CGTTTATCA TGAGGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGGA AAAATATCGA TTGCGCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCG AGAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGAACAAAGA ACATCCCGAA 720
 CCCAAGATTC AGAGGTGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGGTGGCAT ACGCGAGGAA TGAACCTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGCGCCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAA AGGTTGTGG 1200
 GAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAAC 1260
 GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAGAATTT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCCT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
 AAGAAAGCCA AGGAATTCTT AAACACATA AACTCCAAAC TTCCAGGCTT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800

FIGURE 17HH (CONT.)

GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860			
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTGAA	1920			
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCACTT	1980			
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTAA	AGGACTACAA	AGCCATTGGC	2040			
CCTCATGTGG	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100			
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCATATAGGT	AAATTTACTT	2160			
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220			
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGATACA	GAAAGGAGGA	TTTAAAGGTAT	2280			
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GG 2325	//				
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAT	GAG GCC	GCG TTT	AAA GAT	ACA GAA	GAT GGG	ATA 108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GAT	GTT GTC	CTG ATT	GAC CTA	AAT CTC	CCG 162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GAA CCA	GAA ACA	ATT GGA	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA	GGA ACT	GCA ACA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	CTT GGA	GAA GTC	CTA AAA	GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	TTT AAA	GGA CTT	GGA AAG	GCC GAT	GAA 648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GAT GAA	GAG TGA		

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein

FIGURE 17II (CONT.)

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)
 Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	CGGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCTTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAAG	720
ATGCAGAGTG	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGAG	GACTGGAGAG	AGTTGCAAAG	TATTCATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGTTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTTGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAC TGGAG	GAAAAGTTCTG	GGTTCAAAGT	CTTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCACG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCTGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAAGGA	GGGACTGGAG	CGAAATAGCC	1860

FIGURE 17II (CONT.)

AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920			
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980			
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040			
GTGCGGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100			
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160			
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220			
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAAG	AAGACCTCAG	GTGGCAGAAG	2280			
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328			
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GTT	GTC CTG	ATT GAC	CTA AAT	CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GTT	GAA CCA	GAA ACA	ATT GGA	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC AAC	TTC TTA	GAG ATA	ACA ATT	CAA GGA	ACT GCA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	CTT GGA	GAA GTC	CTA AAA	GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GTT	AAA GGA	CTT GGA	AAG GCC	GAT GAA	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17JJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GGT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC	360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT	420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	600
AAAGATCCCG ATGTATAAT TACCTAACAC GGCAGTTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGGCCG AAAAGTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG	900
ACTGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAACGTAC	960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC	1020

FIGURE 17JJ (CONT.)

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CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCA GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAAC'TGGAG GAAAAGTTTCG GGTTCAAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCTT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCTTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

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Figure 17KK

JDF-3 - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17KK (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCCCGAGAAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACCGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
 ACGCGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCCGGAGAGGCACGGTCGTTAAGTTAAAGCGCGGAGAAAGGTGAAGAAAAAGTTCTCTCGG
 CAGGTCGTGGAGGTCGTGGTCTCTACTTACGCAACCCGAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCAACCCCGGTTCATCGACATCTACGAGTACGACATACCC
 TTTCGCCAAGCGCTACCTCATAGACAAGGGCTTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCTTCCGATCGAGACGCTTACCA CGAGGGAGAAAGATTGGAA
 CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTTGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAGGAGATGATTAA
 GCGCTTCTTGAGGGTCGTTAAGGAGAGGACCCGACGTCGTGATAACATACAAACCGCGACAACTTCGACTTCGCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
 ACCCTCGGAGGGACGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTTCGAGTGAAGGCGAGGTACA CTTCGACCTTTATCCAGTCTAAAGCGCA CCATAA
 ACCTCCCGACCTACACCTTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGAGATAGCCA CCGCTGGAGACCGGCGAGGGCTTGAGAG
 GGTCCGCGCTACTTCGATGGAGGACCGAGGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGGCGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
 CGCTCCAGCACCGGCAACTCTGTCGAGTGGTCTCTCTAAGGAAGGCTACGAGAGGAACGAACCTCGTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
 ACGCGGTGGTACGTCAGGACCGGAGCGGGGACTGTGGGCAATATCGTGTATCTAGACTTTCGTTAGTCTCTA CCTTCAATCATAA TCAACCA CAACGCTCTGCCAGATAC
 GCTCAACCGCGAGGGGTAGGAGCTACGAGCTTGGCCCCCGAGGTCGAGTCAAGTTCTGCAAGGACTTCCCGGCTTCATCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
 CAGAAGATAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGATCTCTCGATTACAGGCAACGCGCTATCAAGATTCTCGCCAACAGCTACTACGGCTACGAGCT
 ATGCCAGGGCAAGATGGTACTGCAGGAGTGCCTGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAGTTCGGTTTAAAGTCTCT
 CTATGCAGACACAGACGGTCTCCATGCCACCATCTCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTCTTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
 GAACCTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCA CCGCGGGCTTGAGATAGTCAGGCGCG
 ACTGGAGCGAGATAGCGAAGGAGACGCGAGGAGGGTCTTGGAGGCGATAC TCAAGGACTCAAGGCCACCGGCCCGACGTTAGCCATAGCGAAAGCGTTTGGCCCGCAGAGGT
 GTACGAGGTTCCCGCGGAGAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTCAAGGCCACCGGCCCGACGTTAGCCATAGCGAAAGCGTTTGGCCCGCAGAGGT
 GTTAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCAAAAGTACGATG
 CGGACTACTACATCGAGAACCAGGTTCTGCCCGCAGTTGAGAGAAATCTCTCAGGGCTTTCGGCTACCGCAAGGAAGACCTTCGCTACCGAAGACGAGGCGAGTTCGGGCTTGGCGC
 GTGGCTGAAGCCGAAGGGGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GAT GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC ATG GAT CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648

FIGURE 17KK (CONT.)

GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17LL

(PCNA) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC
 CTACTTCTACGCGCTCCTCAGGGACGACTGTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAAGGTGA
 AGAAAAAGTTCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTTCACGCACCCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTCA TC
 GACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACGATCGA
 GACGCTCTACCCACGAGGAGAAAGAGTTTGGAAACCGGGCCGATTCTGTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTC

113/186

Figure 17MM

Sac7d_gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 70)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S	18
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GTA	GAC	ACT	TCA	54
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D	36
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC	108
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L	54
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA	162
L	D	M	L	A	R	A	E	R	E	K	K	*						67
TTA	GAC	ATG	TTA	GCA	AGA	GCA	GAA	AGA	GAG	AAG	AAA	TAA						201

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GTA	GAC	ACT	TCA
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA

REPLACEMENT SHEET

FIGURE 17NN (CONT.)

```

L D M L A R A E R E K K //
TTA GAC ATG TTA GCA AGA GAA GAG AAA AAG AAA //

      G G G
      // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K

```

REPLACEMENT SHEET

FIGURE 17NN (CONT.)

GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G GCG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 CTG GCC GCG AAG GAG GCG CGG GGC CTT CTC GGC AAA GAC CTG AGC GTT CTG
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGC CTT CTC GGC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGC GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

REPLACEMENT SHEET

FIGURE 17NN (CONT.)

A N L W G R L E G E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

FIGURE 17NN (CONT.)

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Figure 1700

Taq DNA polymerase- Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

```

      G   G   G
      // GGC GGC GGT

V   T   S   G   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
```

REPLACEMENT SHEET

FIGURE 1700 (CONT.)

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CCG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG GGC GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

REPLACEMENT SHEET

FIGURE 1700 (CONT.)

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y

REPLACEMENT SHEET

FIGURE 1700 (CONT.)

ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

FIGURE 1700 (CONT.)

L S A K E G I D G R G G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT CAT
H H //
CAT CAT //
M V K K V K F K Y K G E E K E V D T S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
K I K K V W R V G K M V S F T Y D D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
N G K T G R G A V S E K D A P K E L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
L D M L A R A E R E K K // *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)

//
ccctggctct ggggccacat atatgttctt actgcctttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gtttttact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga

FIGURE 17PP (CONT.)

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctctttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagcctaaa gattcttggc ttcgatatag aaacctctta
tcacgaagga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gattttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgttttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggtcaggg agagctacac

FIGURE 17PP (CONT.)

aggtagattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctoga ttataattac ccacaatgtt tctcccata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatatag gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaaga gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cagtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcgggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct

FIGURE 17PP (CONT.)

aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttccccacc caagtccgct
acaatttttt ccttgatatct cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnga
aagattgaga tgttcttgg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

FIGURE 17PP (CONT.)

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //TGA

Figure 17QQ**Sac7d - Pfu DNA Polymerase (WT) fusion protein**

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //
//
ccctggctct ggggccacat atatgttctt actcgccctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aagggttgaga aaaagtttct cggcaagcct attaccgtgt ggaacttta
tttgggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaaatcg atattccatt tgcaaaagaga tacctcatcg acaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttgatatag aaacctcta
```

FIGURE 17QQ (CONT.)

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggagaagt acatttcgac ttgtatcatg taataacaaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaacccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgttttcaag
gtcaagcaca gggaaacctg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtaggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaaagac
aaaaatgaag gaaactcaag atccctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

FIGURE 17QQ (CONT.)

gaaggagctc gaagaaaaagt ttggatttaa agtcctcttac attgacactg atgggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaaga ccattacatg agtataaggc gataggtoct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctacattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaacttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgcgac gtagatcttt

FIGURE 17QQ (CONT.)

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tttgctccaa gcagagccgc tccaatggat aacacccctg ttccccgacc caagtccgct
acaatttttt ccttgatatc cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacctcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttg // TGA

```

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17RR (CONT.)

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

 ATGATTTTATG ATGTGGATTAT CATAACTGAA GAAGGAAAAAC CTGTTATTATG GCTATTCAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACATT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA AGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCCTG ACATTTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
 AAAAGGGCAG AAAAATCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGNATACA TTTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGAGAGAG ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT AACCTTGTAG AGTGGTTCTT 1020
 TTATGGGATG TTTTCAAGGTC AAGCACAGGG AAGCTTGTAG AGTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAAG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTG TAATTTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGCGG TTAGTGCCTG GGAAGAGAAAG 1560
 TACATCGATG TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAA TTTGTAATAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCTGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTTACTCG TGGTTTATAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAAATAG TAAAGAGAGT AATACAAAAG CTTTGCCAAAT ATGAAATTTCC ACCAGAGNAG 1980

FIGURE 17RR (CONT.)

CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGAATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
 // TGA

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAAG GAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATTA CATTTACGCT 120
 CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXX CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGATTCCC ATATTAGCG 660
 AAAGGGGAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGAGGAGAA TAGCGGATAT GACGGCTGTA AAGTCAAGG GAAGATACA TTTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAITCCT TCCAATGGAA ATTTCAGCTTT CAAGATTAGT TGGACAACCT 1020

FIGURE 17SS (CONT.)

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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

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Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)
 Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17TT (CONT.)

G387p Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGAT ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGNAATCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAAT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAAG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAT AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATC TAAATCTTGA GGGATGCAAG AACATATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGTCCCTG GACTGTGATA GCTTGAATAT 1740
GAAGGTTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATACTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCCAAT ATGAAATTTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCTAC 2040

FIGURE 17TT (CONT.)

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GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCITCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
AGAGAACATC CAGCATTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420

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FIGURE 17UU (CONT.)

GATATAGAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTGAAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAT TCGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGCGAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAG CGAGCCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAACTCAAGG GAAAGAATACA TTTCCGACTTG 780
 TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGNAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGAGAGAG ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACCTTAT 960
 GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACTT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAGG 1140
 CTCAGGGAGA GCTACACAGTTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
 AAGTTCCTGA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGNA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGTACTG TAAGGAGTGT GCTGAGAGCG TTAATGCGCTG GGGAGAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CTTCTACAT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAA TTTGTAATAA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAGAGCT 1920
 GTGAGAAATAG TAAAGAGAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAG 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAT 2100
 GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17VV

SAC7D-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTATG ATGTGGATTA CATAACTGTA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTTAA GATAGAGCAT GATAGAAGCTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGGAG GTTGAGAAAA AGTTTCTCGG CAAAGCCTATT 240
ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAAGATXXXIC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAA AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAAATGAA ATTCAAGCTTT CAAGATTAGT TGGACAACTT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGAGTA TCAAAGAAGG 1140

FIGURE 17VV (CONT.)

CTCAGGGAGA GCTACACAGTTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTAA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
 AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATTCCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGTTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17WW**KOD DNA POLYMERASE - Sac7d fusion protein**

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCAATAG AATTTTCAAG 60
 AAGGAAAACG CGGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTTCTACGC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAAGT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAGATA 300

FIGURE 17WW (CONT.)

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGGAATTAGT GCCAATGGAA GGGGACGAGG AGCTGAATAAT GCTCGCCTTC 420
 GACATTGAAG CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CTTATGATA 480
 AGCTACGCCG ACAGGAAGG GGCACGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
 GTTACGTCG TCTCCACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCG ACCTTCTCAT AACCTACAC GGCACAACT TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGT AAAAGCTCGG AATAAACTTC GCCCTCGGA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGGCACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGTTGAGGC CGTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACAC AGCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTTCTT CCTCAGGAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAGC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAG CTATGTAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGTACT ACGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTTGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACGCGGCTT CTTCTGTCAG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGAGGACG GTGACGTCGA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGC GGAGAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGCACTACA AGGCAACCG TCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATGTCG TCAAGGGCTC TGGGAGGATA GGCACAGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACGAGT TCTCCCAGCC 2220
 GTTGAAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
 // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17XX

Sac7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATCTCTCG ACACGTGACTA CATAACCGAG GATGGAAGC CTGTCAATAAG AATTTTCAAG 60
AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAGA TAACCGCGA GAGGCACGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAAGTT 240
GAGGTCTGGA AACTTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCG CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTTCGCC AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAG CGAGCCGAAG 720
ATTCAAGAGG TGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGTTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCTGGGAA 900
ACCGGCGAGA ACGTTGAGAG AGTCGCCCG TACTCGATGG AAGATCGGAA GGTCACTAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTGCTTAAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGTCT CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTATGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260

FIGURE 17XX (CONT.)

GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CCGCTATGCA 1500
 AGGGCGGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCTGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGCA GAAAGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCAG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTC TCAAGGGCTC TGGGAGGATA GGCACACGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTCCGTTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17YY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

ATGATACTGG ACACGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCTATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180

FIGURE 17YY (CONT.)

AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTACAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXK CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
 GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGAACACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCITTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAG ACCGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AATCCACAA TTGACCCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGGCTT TAAGGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTAATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCCCT AAACCTACATA AACCTCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACGTGTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCAATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGTCTGA TGCAGTGAAA GTGAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCAATTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
 GATATTGAAA CGTTTATCA TGAGGGAGAT GAAATTGGAA AGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGGA AAAATATCGA TTGCCCCTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCCGCTT GTCITTAGGA GGGACAAAAG ACATCCCGAA 720
 CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACITT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTtagGAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGTTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAA AGGTTTGTGG 1200
 GAAAATATCA TTTTATTTTGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTCACAA 1260
 GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTTATCCCT CCATACCTCG GGACTTAAAT 1380

FIGURE 17ZZ (CONT.)

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GCAATGAGGC AAGATATATAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCCT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
```

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17AAA (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)	
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)	
ATGATACTTG ACCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTCAAAG	60
AAAGAAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT	120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCCCGA GAGGCATGG	180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGG GAGGCCGATT	240
GAGGTATGGA GGCCTGTACTT TGAACACCCCT CAGGACXXIC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC	360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCATGAAG AGCTCAAAGT GCTCGCATTT	420
GACATAGAAA CCCTCTATCA CGAAGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACTGGGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGTAG TTTCCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAAGT GATAAGGAG	600
AAAGATCCC ATGTTATAAT TACCTACAAC GCGCATTTCT TCGACCTTCC CTATCTAGTT	660
AAGAGGGCCG AAAAGCTCG GATAAAGCTA CCCCTGGGA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGC TTGGGGATAT GACAGCGTG GAGATAAAG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGG AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGAG	900
ACTGAAAAGG GACTGGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAAACGTAC	960
GAGCTCGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAAGTTAGT CGGCCAGCCC	1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGTGG AGTGTACCT CTTCAGGAAG	1080
GCCTACGAGA GGAATGAAT GGCTCCAAAC AAGCCGAGT AGAGGAGTA CGAGAGAAG	1140
CTAAGGAGA GCTACGCTGG GGGATACGTT AAGAGCCGG AGAAAGGGCT CTGGAGGGG	1200
TTAGTTTCCC TAGATTTTAC GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA	1260
CCGATACGC TGAACAGGA AGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC	1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGA	1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT	1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAACAGCT ATTATGGGT TTTATGGGTAC	1500
GCAAAAAGCCC GTTGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA	1560
TATATAGAGT TCGTAAGGA GGAATGGAG GAAAAGTTCC GGTTCAAAAGT CTTATACATA	1620
GACACAGATG GACTTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAA	1680
GCCCTAGAGT TCGTAGATTA TATAACGCC AAGTCCAG AGCTGTGGA GCTTGAGTAC	1740
GAGGCTTCT ACGTAGAGG GTTCTTCGTG ACGAGAAGA AGTATGCGTT GATAGATGAG	1800
GAAGGGAACA TAATCATAG GGGCTTTGAA ATAGTACGGA GGGACTGGAG CGAAATAGCC	1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGT ATCTAAAGC ATGGCAACGT TGAGGAGGCA	1920
GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAGAT ACAGAAATACC TCCAGAAAAG	1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTTACAGAT ACAAGGCTAT AGGTCCGCAC	2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA	2100
GGGTACATAG TGCTAGGGG AGACGGGCCA ATAAAGCAAGA GGGCTATCCT TGCAGAGGAG	2160

FIGURE 17AAA (CONT.)

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TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAATCA GGTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA
```

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)
 Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
 AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
 CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTCTGG GAGGCCGATT 240
 GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXX CCGCAATAAG GGATAAGATA 300
 AGAGAGCAAT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
 CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCATGAAG AGCTCAAGTT GCTCGCATTT 420
 GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCCGGA AGGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGGTAG TTTCCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
 AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTTCTT TCGACCTTCC CTATCTAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
 ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
 TACCACGTGA TTAGGAGAAC GATAAACCTC CCNACATACA CCCTCGAGGC AGTTTATGAG 840
 GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
 ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAACGTAC 960
 GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
 CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
 GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
 CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAGGGCT CTGGGAGGGG 1200
 TTAGTTTCCC TAGATTTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCTA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGCGGCAC 1320

FIGURE 17BBB (CONT.)

```

AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACCTGGG GAAAAATTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGGAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTAGAGG GTTCTTTCGTG ACGAAGAGA AGTATGCGTT GATAGATGAG 1800
GAAAGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACC AAGCAAAAGT CCTAGAGGT ATCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAG CTGAGCAAAGT ACGAATACC TCCAGAAAG 1980
CTAGTTATTT ACGAGCAGT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA 2100
GGGTACATAG TGCTAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCTTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

```

Figure 17CCC**JDF-3 - Sac7d fusion protein**

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATGATCCTTGACGTTGATTACATCCGAGAATGGAAGCCCGTCTATCAGGGTCTTCAAGAAGAGAA CGGCGAGTTCAGGATTGAATACGACC GGAGTTCGAGGCCCTACTTCT
ACGCGTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGAGAGGCA CGGCAAGGTCTTAAGGTTAAGCGCGGAGAGGTGAAGAAAAAGTTCCCTCGG
CAGGTTGTGGAGGTCCTGTCCTCTACTTCACGCACCCGAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACC CGCGGTCTACGACATCTACGAGTACGACATACCC
TTGCCAAGCGTACCTCATAGACAAGGCCCTATCCCGATGGAGGTGAGGAAGAGCTTAACTCATGTCTCTTGAGTATCGAGACGCTCTACCCAGGGAGAAGAGTTGGAA
CCGGGCCGATTCTGATGATAGCTACGCCGATGAAGCGAGGCGCGGTGATAACCTTGAAGAGATCGACCTTCTTACGTTGAGGTTGTCTCTCCACCAGAGAGGAGATGATTAA
GCGCTTCTTTAGGGTCGTTAAGGAGAAGGACCCGACGTCTGTGATAACATACACGCGCA CAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCTTT
ACCTCCGGAGGACGGGACGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCTGAGGTGAAGGGCAGGGTACACTTCGACCTTTTATCCAGTCTAAGGCGCACCATAA
ACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCCGAGGAGATAGCCACCGCTGGGAGACCGGCGGCTTGAGAG

```


FIGURE 17CCC (CONT.)

GGTCGGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
 CGCTCCAGACCGGCAACCTCGTCGAGTGTTCTCTAAGGAGGCTACGAGAGGAACGAACCTCGTCCCAACAAGCCGACGAGAGGAGCTGGCCGAGGAGAAGGGGGGCT
 ACgCGTGGCTACGTCAAGGACCGGAGCGGGACTGTGGACAATATCGTGTATCTAGACTTTTCGTAGTCTCTA~~CC~~TTCAATCATATCACCACAACGTCCTCGCCAGATAC
 GCTAACCGCGAGGGGTGTAGGACTACGACGTTGCCCGAGGTCCGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
 CAGAAGATAAGAGGAAGTGAAGGCACTCTCGACCCCGTGGAGAGGATCTCCTCGATTACAGGCAACG~~GC~~ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
 ATGCCAGGGCAAGATGGTACTGCAAGGAGTGC CGCAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCCT
 CTATGCAGACACAGACGGTCTCCATGCCACCATTTCTTGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
 GAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCGTACGAAGAAAAAGTACGCGGTCAATCGACGAGGAGGCAAGATAACCAACGCGCGGCTTGAGATAGTCAGGCGCG
 ACTGGAGCGAGATAGCAAGGACGCGAGGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTTGAAGAGGCCGTCAGAAITGTCAAGGAAAGTCACCGAAAAAGCTGAGCAA
 GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGACGTAGCCATAGCGAAgCGTTTGGCCCGCAGAGGT
 GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGACAGGGCGATTCCCTTCGACGAGTTCCGCCGACGAAGCAAAAGTACGATG
 CGGACTACTACATCGAAGAACCAAGGTTCTGCGGCGAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAAGAAACGAGGACAGGTTCGGGCTTGGCGC
 GTGGCTGAAGCCGAAGGGGAAGAAG//

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

150/186

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71)

Amino acid sequence (SEQ ID NO: 72)

```
A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L   Q   M   L   E   K   Q   K   K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
// A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L   Q   M   L   E   K   Q   K   K   //   G   G   G
CTG CAG ATG CTG GAG AAG CAG AAA AAG //   GGC GGC GGT
```

REPLACEMENT SHEET

FIGURE 17FFF (CONT.)

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG CTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D

REPLACEMENT SHEET

FIGURE 17FFF (CONT.)

GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
CTG GCC GGC AGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC

REPLACEMENT SHEET

FIGURE 17FFF (CONT.)

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CTC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

FIGURE 17GGG (CONT.)

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctctttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaatttgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagAAC atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcAAAagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaaggA gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaacccttga
gagagttgcc aaataactga tggaaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaaccttg tagagtgtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

FIGURE 17GGG (CONT.)

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc ctigactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttta agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgttggtta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgaatgg ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcgggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttctctg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tggttaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

REPLACEMENT SHEET

FIGURE 17GGG (CONT.)

```

tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaaaggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctocaa gcagagccgc tccaatggat aacacccctg ttccccgacc caagtccgct
acaatttttt ccttgatatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaaact ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttg //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGG AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA CCAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGAG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

FIGURE 17HHH (CONT.)

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GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

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Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTGAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTTGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GATTTTGGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAATCTGG GATTAAATTA ACCATTGGA AGATGGAAG CGAGCCCAAG 720

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FIGURE 17III (CONT.)

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ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTACGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAAGG AACCTTGTA AGTGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAA 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCITACGGATA TTATGGCTAT 1500
GCAAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAA TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGAATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

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// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

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Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17JJJ (CONT.)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCGAG AAAAATTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAAT AGTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
AAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AACTTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220

FIGURE 17JJJ (CONT.)

GCGGTACTTA GGATATTGGA GGAATTGGG TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
 // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17KKK**KOD DNA POLYMERASE - Sso7d fusion protein**

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71)
 Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATCCTCG ACATGACTA CATAACCGAG GATGGAAGC CTGTCAATAAG AATTTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTCTACGCC 120
 CTCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGG 180
 ACGGTTGTAA CCGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCG GAGACCAGTT 240
 GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTATAGACA AGGGAATTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
 GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAACT TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GCGATGGAAG CGAGCCGAAG 720
 ATTACAGAGG TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAAG AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACTAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTGCTTTAAT CGGCCAGTCC 1020
 CTCTGGGAG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTCTCT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380

FIGURE 17KKK (CONT.)

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CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GTCCTCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGTACTT ACGTTACTA CGGCTATGCA 1500
AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGTACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCTGTC TCAAGGGCTC TGGGAGGATA GGCACACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCTGTTAC CGCAAGGAAG ACCTGCCGTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG //

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FIGURE 17LLL (CONT.)

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//ATGATCTCG ACACTGACTA CATAACCGAG GATGGAAGC CTGTACATAAG AATTTCAAG 60
AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCCTC 420
GACATTGAAA CTCCTTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGGA TCTCCCTTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GGCACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTACAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGGGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATCGGAA GGTCAACATAC 960
GAGCTTGGGA AGGAGTTTCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGCGGCTT CTTCTGTCACG AAGAAGAAGT ATCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGACAG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTGCA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTAC AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCAG AGCAGATTAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGGCTC TGGGAGGATA GGCACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

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Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTGG ACACGTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGTCTATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGAGT AGTCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAAATATCA TTTTATTTTGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAAC 1260
GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTTATCCCT CCATACCTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCCGAT CGAAAAAGAA 1440

FIGURE 17MMM (CONT.)

ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTTAA 1680
 AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGG TTGGAAGTAG TAAGGAGAGA TTGAGTGAG 1860
 ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGTAA GCGATAGGGT AATTTTACTT 2160
 ACAGAAATCG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTACAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGTCAATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCCTT 420
 GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840

FIGURE 17NNN (CONT.)

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TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTTATTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCTT AAACATACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGAATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
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// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17O00

Deep Vent- Ssod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17000 (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)			
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)			
ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC
AAAGAAAACG	GGGAGTTTAA	GGTTGAGTAC	GACAGAAACT
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA
GAGGTATGGA	GGCTGTACTT	TGACACACCT	CAGGACXXXC
AGAGAGCATT	CCGCGATTAT	TGACATCTTT	GAGTACGACA
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA
GTGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT
AAGAGGGCCG	AAAAGCTCGG	GATAAAGTCA	CCCCTGGGAA
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA
GCAATCTTCG	GAAAGCCAAA	GGAGAAAAGT	TACGCTCAGG
ACTGGAAGAG	GACTGGAGAG	AGTTGCAAG	TATTTCAATGG
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGT
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTTCG
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG
GAGGGTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA
GAAGGGAAGA	TAGTCACTAG	GGGGCTTGAA	ATAGTCAGGA
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGTT	ATCCTAAAGC
GTAAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA
TTTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA
			AGAAG

2328

FIGURE 17000 (CONT.)

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17PPPSsod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)
 Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

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ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAGAGGGTAC 360
CTAATAGACA AAGGCCATAAT TCCAATGGAA GGCAGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCAGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
```

FIGURE 17PPP (CONT.)

TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAC'TGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACGTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTAATT	ACGAGCAGAT	CACGAGGCC	CTTACAGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGTTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17QQQJDF-3 - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCCGTATCAGGGTCTTCAAGAAGGAGAAACGGCGAGTTCAGGATTGAAATACGACCGGAGTTCGAGCCCTACTTCT
 ACGCGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGACCGCAGGGTCGTTAAGTTAAGCGCGGAGAGGTGAAGAAAAAGTTCCTCGG
 CAGGTCGTGGAGGTCGTGGTCTCTACTTCAACGACCCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCTACGACATCTACGAGTACGACATACCC

FIGURE 17QQQ (CONT.)

TTTCGCCAAGCGTACCTCATAGACAAGGGCCTAATCCCGATGGAGAGTGGAGAGCTTTAAACTCATGTCTCTTCGACATCGAGACGCTCTACACGAGGGAGAAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTTGAAGAAGATCGACCTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GGCTTCTTGAGGGTCGTTAAGGAGAAGACCCGGACGTGTGATAACATACACGGCGACAATTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCTTT
ACCTCCGGAGGGACGGAGCCGAAGATACAGCGCATGGGGACAGTTTTCGGTCCGAGGTGAAGGGCAGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAA
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAG
GGTCGGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGCTCCAGCACCCGCAACCTCGTCGAGTGTCTCTTAAGGAGGCTACGAGAGGAACGAACCTCGTCCCAACAAGCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCT
ACGCGGTGGCTACGTCGAAGGACCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCCGTAAGGACTTCCCGGCTTCATTCGAGGCTGCTCGGAAACCTGCTGGAGGAAAGG
GCTCAACCGGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGTCCGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGGCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCCCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAACACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCGCCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCGTACGAAGAAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCAACGCGCGGGCTTGAGATAGTCAAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGAAGAGCCGCTCAGAAATTGTCAAGGAAAGTCAACCGAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAAGCCACCGGCCCGCACTAGCCATAGCGAAAgcGTTTGGCCCGCAGAGGT
GTAAAAATCCGCCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAAGCAAGTACGATG
CGGACTACTACATCGAAGAACGAGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCTTCGGCTACCGCAAGGAAGACCTCGGCTACCAAGAAGACGAGGCGAGGTTCGGGCTTGCGGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TAG

Figure 17RRR

sso7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

FIGURE 17RRR (CONT.)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCCGTATCAGGGTCTTCAAGAAGGAGAACCGGCGAGTTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCGCGGAGAAAGGTGAAGAAAAAGTTCTCTCGG
CAGGTCGTGGAGGTCTGGTCTCTACTTTCACGCACCCGCGAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGGTCAATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTCTTGAATdGAGACGCTCTACACGAGGAGAAAGAGTTTGGAA
CCGGCCCGATTCTGATGATAAGCTACGCCGATGAAGCGGAGGCGCGGTGATAACCTTGGAAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGGGGTCGTTAAGGAGAGGACCCGGACGTGCTGATAACATACAACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTCGGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGGTCGAGGTGAAGGCGAGGTACACTTCGACCTTATCCAGTCAATAAGGCGCACCATAA
ACCTCCCGACCTACACCTTGGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTTACCTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGCTCCAGCACCCGGCAACCCTCGTCGAGTGGTTCTCTTAAGGAAGGCCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCGACGAGAGGGAGCTTGGCAGGAGAAAGGGGGCT
ACGcCGGTGGCTACGTTCAAGGAGCCGGAGCGGGGACTGTGGACAAATATCGTGTATCTAGACTTTCGTAGTCTTAqCCTTCAATCATAAATCACCAACAGCTCTCGCCAGATAC
GCTCAACCCGAGGGGTGTAGGAGCTACGACGTTTCCCCCGAGGTGCTCAAAAGTTCTGCAAGGACTTCCCCGGCTTCAATCCGAGCTTCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCTCGATTACAGGCAACGqGCCATCAAGATTCTCGCCAAACAGCTACTACGGCTACGGCT
ATGCCAGGGCAAGATGGTACTTGCAAGGAGTGCGCCGAGAGCGTTTACGGCATGGGAAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTTAAAGTCTCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACCGTGAAAACAGTCAAGAAAAAAGCAATGGAGTTCTTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAATCGAATAACGAGGGCTTCTACGTACGGGGCTTCTTCTCGTCAAGAAAGAAAGTACCGGTTCTATCGACGAGGAGGCAAGATAACCAACGCGCGGGCTTGAGATAGTCAGGCGCG
AATGGAGCGAGATAGCGAAGGAGACGCAAGCGGAGGGTTTTTGGAGGCGATACTCAGGCACGGTGACGTTTGAAGAGCGCTCAGAAATTTGTCAAGGAAAGTCAACCGAAAAAGCTGAGCAA
GTAACGAGTTCCGCGGAGAAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCGGCGACGTAGCCATAGCGAAAgcGTTTGGCCCGCCAGAGGT
GTTAAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCCGACGAAGCAAGTACGATG
CGGACTACTACATCGAGAACCAAGTTCTGCGCGCAGTTGAGAGAAATCCCTCAGGGCTTTCGGCTACCGCAAGGAAGACCTCGGCTACCCAGAAGACGAGGCGAGGTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAAGTGA

a

MkTpV	1	valvydaefvgserfefeeeretflk	CVKAYdgvlAERYlmer	SBaKndcEEllelha	73
ReCA	VI		cgnaAlkEYaeVRIdaERlga	fkagdeVvg	74
MkTpV	179	vpIDakeeEEllel	LRendwtpthcEIA	RRGCLSVSeVegckdpessgiylswrvvn	75
HTH	asnC	IDKIdERHlIneL	qkdGRRRISnEIA	RRVGLSVStVrervr	76
HTH	SS				

b

A	299	lkeqdrVCLFEdvAlc	larafdgssismiattpy	Ktlk'vvc	pdltleeeAksVnrtl	77/78
B	354	atLIdenhCLspdaA	deLlEhPeSiaagila	tdlEeiErmyE	ecrlseeAyravei	79/80/81
C	411	aeLtkkeGVGrEta	eElLraFgnperVklare	eeiEklaSe	CVGservlrsilvpgy	82
D	468	asLIsirGLdrera	AerLtkkYGGYskv	reagvEELRE	dGLEdaqlreikg	83/84/85
E	518	lkeLesivGdllek	AdeLkrkYGSasaV	rrlpvEELRE	lGSSddeElaeikg	86/87/88
F	568	iprkLreaGdllet	AaeLyerYGSlskeig	rrlsyddLLE	lGatpkAaeikgpe	89/90/91
G	622	kfLlnieGVGpELa	EElLeaVdydleEl	aslnpEELaEVE	GlGeeLaeVvyaa	92/93
H	696	wkeLlerkVGegrA	rrLleyFGSageVgklven	aeVskll	VpGlGdeavarlvgg	94/95
I	752	ykELrdaGLtpae	AervLkrYGSvskvq	egatpdeLRE	lGlgdakarllg	96/97/98
J	803	lrELvnkELdvdtA	YelLkrYGSvsaV	rkApvkeLRE	lGlsdrkharikgip	99/100/101
K	855	etmLqvrGmsveka	erLterFdtwtkv	keApvsaELV	VpGVGlsilvkeikagv	102/103/104
L	912	kaLldvkGVepela	drLveeLGSpyrv	ltaKksdlm	VerVgpklaerlraag	105/106/107
ECRuVA	73	keLlktngGVGpklA	laElsgmsaqgfV	naVerEEVgalp	GlGkktAerlIivem	108/109
HsPolB	57	aeakklpGVGtEiA	Ekldeflategklr	klekirqddtss	ivsglGpsaaArkEvddeg	110
TaqPol	93	levmevppGVGpktA	rglYeaLGlalsle	klkealergdl	lKGlGackkAerlkegl	111/112/113
Consensus		uu gvg A ll ygs u	eu eu gug u			
HhH	SS					

FIGURE 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGCTACTAGTCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGAAGGGGGCC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCCTGTGGGCCGATCTTCTGGCCCT
GGCCCGCCGAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCAACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAAGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCCCTTCCGCTGTCTGGGCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
GGACCAGCTGGAAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGCTCCACGAGCGCCGCTCTGGAGGCCCTCCG
CGAGGCCACCCCATCGTGGAGAAGATCCTGCACTACCGGGAGCTACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCGCTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACAGGAGACCGCCAGCTGGATGTTCCGGCTCC
CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCTCTACGGCATGTGCGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCTGGAGGAGGGCAGGAGGCGGGGTACGTGGAGAC
CTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCTCGAGGCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGCGGAGGCGGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGVTSFKALEEAPWPPPEGAFFVGFVLSRKEPMWADLLALAA

FIGURE 19 (CONT.)

ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
 SNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERPLS
 AVLAHMEATGVRDLVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
 DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
 PRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDYS
 QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
 LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFGRR
 RYVPDLEARVKSUREAAERMAFNMVQGTAAADLMKLAMVKLFPRLEEMGARMMLL
 QVHDELVLAPKERAEEAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
 GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
 GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
 TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAAG
 GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
 TGTCCTAGTGGGATGCTGCCCCCTCTTTGAGCCCAAGGGCCGGGTCTCTCTGGTG
 GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
 GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
 CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
 CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG
 AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
 GGCGCGCTCGAGGTCCCAGGCTACGAGGCGGACGACGTCTGGCCAGCCTGGC
 CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
 ACCTTTACCAGTCTCTTTCCGACCGCATCCACGTCTCCACCCCGAGGGGTACCT
 CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCCGACCAGTGGGC
 CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
 CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
 CCCTCCTCAAGAACCTGGACCGGTGAAGCCCCGCATCCGGGAGAAGATCCTGG
 CCCACATGGACGATCTGAAGCTCTCTGGACCTGGCCAAGGTGCGCACCGACCT
 GCCCCTGGAGGTGAGCTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
 GGCTTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
 GAAAGCCCCAAGGCTCTGGAGGAGGCCCCCTGGCCCCCGCCGAAGGGGCCTTC
 GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
 CCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
 GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
 TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCT
 CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
 GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTCCGAGAGGCTCTTCGCCAA
 CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
 GGAGAGGCCCTTTCCGCTGTCTGGCCACATGGAGGCCACGGGGGTGCGCCT
 GGACGTGGCCTATCTCAGGGCCTTGTCCTGGAGGTGGCCGAGGAGATCGCCCG
 CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
 GACCAGCTGGAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
 ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCTGGAGGCCCTCCGC
 GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTACCAAGCTG
 AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGGCCGCC
 TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
 ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
 GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
 AGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
 CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGGCGTCCCC
 CGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
 GTCCTCTACGGCATGTGCGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTACG
 AGGAGGCCACGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCCGCCGCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTGATGGAGGGGGTGTATCCCC
TGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGSVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFASLLKALKEDGDAVIVVFDKAPSFRHEAYGGYKAGRPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRLTADKDLYQLSDR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGETARKLL
EEWGSLEALLKNLDRPKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLELLEFGSLLEHFGLESKALEEAPWPPPEGAFVGVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSDPNLQNPVRTPLGQIRJRRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPEYEEAQAFIERFYQSFQKVRWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKSUREAERMAFNPVQGTAAADLMKLAAMVKLFPRLEEMGA
RMLLQVHDELVLAPKERAEEAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHHH

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTATAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAATAATTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGCACTTGTATCATGTAAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTTCGTTAAAGAGCCAGAAAAGGGGTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
 TTAGCAAATTCCTTTCTACGGATATTATGGCTATGCAAAGCAAGATGGTACTGTA
 AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
 GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG
 GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
 TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
 TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
 AGATGAAGAAGGAAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
 GAGTGAAATTGCAAAAGAACTCAAGCTAGAGTTTTGGAGACAATACTAAAAACA
 CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
 CAATTATGAAATTCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
 ATTACATGAGTATAAGGCGATAGGTCTCACGTAGCTGTTGCAAAGAACTAGCT
 GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
 GCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCCAA
 AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCAGCGGTA
 CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG
 ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC
 GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
 CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
 GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAAGGACGCGCC
 GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERH
 GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
 KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKND
 LPYEVVSSSEREMIKRFLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
 EPKMQRIGDMLAVEVKGRIFDLHYHVTIRTNLPYTYLEAVYEAIFGPKPEKVYADEI
 AKAWESGENTLERVAKYSEMEDAKATYELGKEFLPMEIQLSRLVGGPLWDVSRSTGN
 LVEWFLLRKAYERNEVAPNKPSEEEYQRRLESYTGGFVKEPEKGLWENIVYLDIFR
 ALYPSIIITHNVSPDTLNLGCKNYDIAPQVGHKFKCDIPGFPSLLGHLLEERQKIKTK
 MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
 LVWKELEEFKFKVLYIDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYE
 GFYKRGFFVTKRYAVIDEEGKVITRGLIVRRDWSEIAKETQARVLETILKHGDVEE
 AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
 MVIGYIVLRGDPISNRILAEEDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
 LRYQKTRQVGLTSWLNKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGMIS
 FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

atgattacga	attcgacggt	gaaggtaaag	ttcaagtata	aggggtgaaga	gaaagaagta
gacacttcaa	agataaagaa	ggtttgagaga	gtaggcaaaa	tggtgtcctt	tacctatgac
gacaatggta	agacaggtag	aggagctgta	agcgagaaag	atgctccaaa	agaattatta
gacatgttag	caagagcaga	aagagagaag	aaaggcggcg	gtgtcactag	ccccaggcc
ctggaggagg	ccccctggcc	cccgccgga	ggggccttcg	tgggctttgt	gctttccgc
aaggagccca	tgtgggcccga	tcttctggcc	ctggccgccc	ccaggggggg	ccgggtccac
cgggcccccg	agccttataa	agcctcagg	gacctgaagg	aggcgcgggg	gcttctcgcc
aaagacctga	gcgttctggc	cctgaggga	ggccttggcc	tcccgcggcg	cgacgacccc
atgctcctcg	cctacctcct	ggaccttcc	aacaccaccc	ccgagggggg	ggcccggcg
tacggcgggg	agtggacgga	ggaggcgggg	gagcgggccg	ccctttccga	gaggctcttc
gccaacctgt	gggggaggct	tgagggggag	gagaggctcc	tttggtttta	ccgggagggtg
gagaggcccc	tttccgctgt	cctggccccc	atggaggcca	cgggggtgcg	cctggacgtg
gcctatctca	gggccttgct	cctggagggtg	gccgaggaga	tcgcccgcct	cgaggccgag
gtcttcggcc	tgcccgggcca	cccttcaac	ctcaactccc	gggaccagct	ggaaaagggtc
ctctttgacg	agctagggct	tcccgccatc	ggcaagacgg	agaagaccgg	caagcgctcc
accagcgccg	cgctcctgga	ggccctccgc	gaggccacc	ccatcggtga	gaagatcctg
cagtaccggg	agctcaccaa	gctgaagagc	acctacattg	acccttgcc	ggacctcatc

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caccccagga cgggcccgcct ccacaccgc ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgtc tgggcagagg
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag
gaggggaggc acatccacac ggagaccgcc agctggatgt tcggcgctccc ccgggaggcc
gtggaccccc tgatgcgccg ggcggccaag accatcaact tcggggctct ctacggcatg
tcggcccccacc gctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt
gagcgctact ttcagagctt ccccaagggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc ggggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagacctc
gagggccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggtc caccgacgagc tggtcctcga ggcccaaaa
gagaggggcg aggcctggc ccggctggcc aaggaggtca tggagggggg gtatcccctg
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc
attgatggcc gcggcgagg cgggcatcat catcatcatc attaa

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SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGMVSFTYDDNGKTGRGAVSEKDA
 PKELLDMLARAEREKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
 AAAGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
 DPSNTTPEGVARRYGGWEETEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
 LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
 LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPLDI
 HPRTGRLHTRFNQTATATGRLSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDY
 SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
 VLYGMSAHLRSQELAIPEYEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFG
 RRYVPDLEARVKSREAAERMAFNMPVQGTAAADLMKLMVKLFPRLEEMGARM
 LQVHDELVLAPKERAEEAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKEGIDG
 RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
 GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
 AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
 GCAAGATGATCTCCTTACCTACGACGAGGCGGTGGCAAGACCGGCCGTGGTG
 CGGTAAGCGAAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
 AAAAAGGGCGGCGGTGTCAACAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
 CCGCCGAAGGGGCTTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
 CCGATCTTCTGGCCCTGGCCGCCGAGGGGGGGCGGGTCCACCGGGCCCCCG
 AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGCTTCTCGCCAAAG
 ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
 CATGCTCCTCGCCTACCTCCTGGACCTTCCAACACCACCCCGAGGGGGTGGCC
 CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGAGCGGGCCGCCCTTTCC
 GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
 TGGCTTTACCGGAGGTGGAGAGGGCCCTTTCCGCTGTCTGGCCCATGGAGG
 CCACGGGGGTGCGCCTGGAGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
 CAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGCCACCCCTTC
 AACCTCAACTCCCGGGACCACTGGAAGGGTCTCTTTGACGAGCTAGGGCTTC
 CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCC
 TGGAGGCCCTCCGCGAGGCCCAACCCATCGTGGAGAAGATCCTGCAGTACCGGG
 AGCTACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACC
 CAGGACGGGCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
 GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCGTCCGCACCCCGCTTGGG
 CAGAGGATCCGCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
 GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAAC
 CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG

ATGTTTCGGCGTCCCCCGGGAGGCCCTGGACCCCCTGATGCGCCGGGCGGCCAAG
 ACCATCAACTTCGGGGTCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
 TAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
 CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
 GGTACGTGGAGACCCCTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCC
 GGGTGAAGAGCGTGC GGAGGCCGAGCGCATGGCCTTCAACATGCCCGTCC
 AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
 GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
 GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
 AGGGGGTGTATCCCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
 ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
 ATCATCATCATTA

SEQ ID NO: 131 The amino acid sequence of PL- ΔTaq fusion protein

MITNSKKKKKKRKKRKKKKKGGGVTS GATVFKFYKGEEKEVDISKIKKVWRVVK
 MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKGGGVTS PKALEEAPWPPPEG
 AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
 ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFAN
 LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVA YLRALSLEVAEEIARLE
 AEVFRLAGHPFNLSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
 EKILQYRELTKLKSTYIDPLDLHPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTP
 LGQRIRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
 GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
 AWIEKTL EEGRRRGYVETLFGRRRYVPDLEARVKS VREAAERMAFNMPVQGTAA
 LMKLAMVKLFPRL EEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
 AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'-CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ ID NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L3035OF 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

Figure 20

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met	Ile	Leu	Asp	Val	Asp	Tyr	Ile	Thr	Glu	Glu	Gly	Lys	Pro	Val	Ile	1	5	10	15
Arg	Leu	Phe	Lys	Lys	Glu	Asn	Gly	Lys	Phe	Lys	Ile	Glu	His	Asp	Arg	20	25	30	
Thr	Phe	Arg	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Arg	Asp	Asp	Ser	Lys	Ile	35	40	45	
Glu	Glu	Val	Lys	Lys	Ile	Thr	Gly	Glu	Arg	His	Gly	Lys	Ile	Val	Arg	50	55	60	
Ile	Val	Asp	Val	Glu	Lys	Val	Glu	Lys	Lys	Phe	Leu	Gly	Lys	Pro	Ile	65	70	75	80
Thr	Val	Trp	Lys	Leu	Tyr	Leu	Glu	His	Pro	Gln	Asp	Val	Pro	Thr	Ile	85	90	95	
Arg	Glu	Lys	Val	Arg	Glu	His	Pro	Ala	Val	Val	Asp	Ile	Phe	Glu	Tyr	100	105	110	
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	115	120	125	
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Ile	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140	
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155	160
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile	165	170	175	
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190	
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	195	200	205	
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220	
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235	240
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255	
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270	

Tyr Thr Leu Glu Ala Val	Tyr Glu Ala Ile Phe Gly	Lys Pro Lys Glu
275	280	285
Lys Val Tyr Ala Asp Glu	Ile Ala Lys Ala Trp Glu	Ser Gly Glu Asn
290	295	300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr		
305	310	315 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu		
	325	330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu		
	340	345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala		
	355	360 365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser		
	370	375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn		
385	390	395 400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr		
	405	410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr		
	420	425 430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly		
	435	440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile		
	450	455 460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu		
465	470	475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly		
	485	490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu		
	500	505 510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu		
	515	520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly		
	530	535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys		
545	550	555 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu		
	565	570 575

Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys			
			580					585					590					
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly			
			595				600					605						
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln			
			610			615					620							
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala			
			625			630				635					640			
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile			
				645				650						655				
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His			
			660					665					670					
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala			
			675				680					685						
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val			
			690			695					700							
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu			
			705			710				715					720			
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn			
				725					730					735				
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg			
				740				745						750				
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser			
			755				760					765						
Trp	Leu	Asn	Ile	Lys	Lys	Ser												
			770			775												

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

ccctggtcct	gggtccacat	atatgttctt	actgcctttt	atgaagaatc	ccccagtcgc	60
tctaacctgg	ggtatagtga	caaattcttc	tccaccaccg	ccaagaagg	ttatttctat	120
caactctaca	cctcccctat	tttctctctt	atgagatttt	taagtatagt	tatagagaag	180
gttttatact	ccaaactgag	ttagtagata	tgtggggagc	ataatgattt	tagatgtgga	240
ttacataact	gaagaaggaa	aacctgttat	taggctattc	aaaaaagaga	acggaaaatt	300
taagatagag	catgatagaa	cttttagacc	atacatctac	gctcttctca	gggatgattc	360
aaagattgaa	gaagttaaga	aaataacggg	ggaaaggcat	ggaaagattg	tgagaattgt	420

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta	480
tttggaaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt	540
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct	600
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta	660
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa	720
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag	780
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat	840
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact	900
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga	960
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag	1020
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc	1080
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga	1140
gagagttgac aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt	1200
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag	1260
gtcaagcaca gggaaacctg tagagtgggt cttacttagg aaagcctacg aaagaaacga	1320
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac	1380
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt	1440
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct	1500
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat	1560
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac	1620
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc	1680
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta	1740
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg	1800
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta	1860
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa	1920
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag	1980
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac	2040
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag	2100
agttttggag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga	2160

agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca	2220
gataacaaga ccattacatg agtataaggc gataggctcct cacgtagctg ttgcaaagaa	2280
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag	2340
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca	2400
caagtatgac gcagaatatt acattgagaa ccagggttctt ccagcggtac ttaggatatt	2460
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aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt	2580
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta	2640
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ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct	2820
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct	2880
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt	2940
tttgctcaa gcagagccgc tccaatggat aacacccttg tccccgcacc caagtccgct	3000
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct	3060
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg	3120
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt	3180
taactttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta	3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc	3300
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta	3360
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa	3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga	3480
aagattgaga tgttcttgg	3499